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OM protein - protein search, using sw model

Run on: June 20, 2005, 16:21:47 ; Search time 29 Seconds
(without alignments)
10.296 Million cell updates/sec

Title: US-09-885-914B-2

Perfect score: 21

Sequence: 1 R1PR 4

Scoring table: BLOSOM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 12390

Minimum DB seq length: 0

Maximum DB seq length: 4

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	4	1	US-08-002-202-10
2	21	100.0	4	3	US-08-481-534-10
3	21	100.0	4	3	US-08-481-534-15
4	16	76.2	4	1	US-08-021-608D-22
5	16	76.2	4	1	US-08-002-202-15
6	16	76.2	4	1	US-08-726-160-22
7	16	76.2	4	2	US-08-685-589A-27
8	16	76.2	4	2	US-08-685-589A-28
9	16	76.2	4	2	US-08-685-589A-29
10	16	76.2	4	3	US-09-400-208B-8
11	16	76.2	4	3	US-09-400-208B-12
12	16	76.2	4	4	US-09-417-608A-88
13	16	76.2	4	4	US-09-400-122A-8
14	16	76.2	4	4	US-09-400-122A-12
15	15	71.4	3	1	US-08-221-582A-1
16	15	71.4	4	1	US-07-906-349A-16
17	15	71.4	4	1	US-08-102-757-23
18	15	71.4	4	1	US-08-167-035-16
19	15	71.4	4	1	US-08-255-272-21
20	15	71.4	4	1	US-08-208-887A-16
21	15	71.4	4	1	US-08-582-257-28
22	15	71.4	4	2	US-08-582-298-28
23	15	71.4	4	2	US-07-963-538B-8
24	15	71.4	4	2	US-08-539-005-16
25	15	71.4	4	3	US-09-320-095-11
26	15	71.4	4	3	US-09-523-487-11
27	15	71.4	4	3	US-08-811-463-37

28	15	71.4	4	3	US-09-388-183-7	Sequence 7, Appli
29	15	71.4	4	3	US-09-280-598-16	Sequence 16, Appli
30	15	71.4	4	4	US-09-933-497B-37	Sequence 37, Appli
31	15	71.4	4	6	5171670-4	Patent No. 5171670
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33	14	66.7	4	1	US-08-102-896-4	Sequence 4, Appli
34	14	66.7	4	1	US-08-280-443-39	Sequence 39, Appli
35	14	66.7	4	1	US-08-457-459-39	Sequence 39, Appli
36	14	66.7	4	1	US-08-555-678-39	Sequence 39, Appli
37	14	66.7	4	1	US-08-478-913-3	Sequence 3, Appli
38	14	66.7	4	2	US-08-685-589A-4	Sequence 4, Appli
39	14	66.7	4	4	US-09-480-718-48	Sequence 48, Appli
40	14	66.7	4	4	US-09-211-715-175	Sequence 175, App
41	14	66.7	4	4	US-09-211-715-176	Sequence 176, App
42	14	66.7	4	4	US-09-211-715-177	Sequence 177, App
43	14	66.7	4	4	US-09-211-715-178	Sequence 178, App
44	14	66.7	4	5	PCT-US95-02275-39	Sequence 39, Appli
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48	13	61.9	4	3	US-08-757-177-1	Sequence 1, Appli
49	13	61.9	4	3	US-08-927-128-10	Sequence 10, Appli
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56	13	61.9	4	5	PCT-US93-06591-4	Sequence 4, Appli
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58	12	57.1	3	1	US-07-816-679A-9	Sequence 9, Appli
59	12	57.1	3	1	US-08-365-759-1	Sequence 1, Appli
60	12	57.1	3	1	US-08-213-897A-12	Sequence 12, Appli
61	12	57.1	3	1	US-08-502-989-6	Sequence 6, Appli
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63	12	57.1	3	2	US-09-439-164-2	Sequence 2, Appli
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66	12	57.1	3	5	PCT-US92-11270-9	Sequence 9, Appli
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69	12	57.1	4	1	US-07-934-553-5	Sequence 5, Appli
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80	12	57.1	4	1	US-08-037-486-5	Sequence 5, Appli
81	12	57.1	4	1	US-08-022-381A-1	Sequence 1, Appli
82	12	57.1	4	1	US-08-171-737-3	Sequence 3, Appli
83	12	57.1	4	1	US-08-095-162-9	Sequence 9, Appli
84	12	57.1	4	1	US-08-225-474-5	Sequence 5, Appli
85	12	57.1	4	1	US-08-365-759-2	Sequence 2, Appli
86	12	57.1	4	1	US-08-365-759-4	Sequence 4, Appli
87	12	57.1	4	1	US-08-202-178-1	Sequence 1, Appli
88	12	57.1	4	1	US-08-202-178-9	Sequence 9, Appli
89	12	57.1	4	1	US-08-049-195A-3	Sequence 3, Appli
90	12	57.1	4	1	US-08-480-367B-44	Sequence 44, Appli
91	12	57.1	4	1	US-08-480-367B-50	Sequence 50, Appli
92	12	57.1	4	1	US-08-076-092-50	Sequence 50, Appli
93	12	57.1	4	1	US-08-076-092-54	Sequence 54, Appli
94	12	57.1	4	1	US-08-238-089-7	Sequence 7, Appli
95	12	57.1	4	1	US-08-487-221A-44	Sequence 44, Appli
96	12	57.1	4	1	US-08-487-221A-50	Sequence 50, Appli
97	12	57.1	4	1	US-08-475-827A-1	Sequence 1, Appli
98	12	57.1	4	1	US-08-480-370-44	Sequence 44, Appli
99	12	57.1	4	1	US-08-480-370-50	Sequence 50, Appli
100	12	57.1	4	1	US-08-102-896-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-08-002-202-10
; Sequence 10, Application US/08002202
; Patent No. 5604201
; GENERAL INFORMATION:
; APPLICANT: Thomas, Gary
; APPLICANT: Anderson, Eric D
; APPLICANT: Thomas, Laurel
; APPLICANT: Hayflick, Joel S
; TITLE OF INVENTION: Methods and Reagents for Inhibiting
; TITLE OF INVENTION: Furin Endoprotease
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti and Witcoff, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/002,202
; FILING DATE: 08-JAN-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5604201nan, Kevin E
; REGISTRATION NUMBER: 35,30003
; REFERENCE/DOCKET NUMBER: 92,448
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-002-202-10

Query Match 100.0%; Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 R1PR 4
Db 1 R1PR 4

RESULT 2
US-08-481-534-10
; Sequence 10, Application US/08481534
; Patent No. 6022855
; GENERAL INFORMATION:
; APPLICANT: Thomas, Gary
; APPLICANT: Anderson, Eric D
; APPLICANT: Thomas, Laurel
; APPLICANT: Hayflick, Joel S
; APPLICANT: Nelson, Jay
; APPLICANT: Stenglen, Stephan G
; TITLE OF INVENTION: Methods and Reagents for Inhibiting Furin
; TITLE OF INVENTION: Endoprotease
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,534
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6022855nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,448-D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-481-534-10

Query Match 100.0%; Score 21; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 R1PR 4
Db 1 R1PR 4

RESULT 3
US-08-481-534-15
; Sequence 15, Application US/08481534
; Patent No. 6022855
; GENERAL INFORMATION:
; APPLICANT: Thomas, Gary
; APPLICANT: Anderson, Eric D
; APPLICANT: Thomas, Laurel
; APPLICANT: Hayflick, Joel S
; APPLICANT: Nelson, Jay
; APPLICANT: Stenglen, Stephan G
; TITLE OF INVENTION: Methods and Reagents for Inhibiting Furin
; TITLE OF INVENTION: Endoprotease
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,534
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6022855nan, Kevin E
; REGISTRATION NUMBER: 35,303

; REFERENCE/DOCKET NUMBER: 92,448-D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; TELEX:
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-481-534-15

Query Match 100.0%; Score 21; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RPR 4
|||
Db 1 RPR 4

RESULT 4

US-08-021-608D-22
; Sequence 22, Application US/08021608D
; Patent No. 5580760
; GENERAL INFORMATION:
; APPLICANT: LEVENS, DAVID L., DUNCAN,
; APPLICANT: ROBERT C., AND AVIGAN, MARK I.
; TITLE OF INVENTION: NOVEL FUSE BINDING
; TITLE OF INVENTION: PROTEIN AND CDNA THEREFOR
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/021,608D
; FILING DATE: 22-FEB-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: WILLIAM S. FEILER
; REGISTRATION NUMBER: 26,728
; REFERENCE/DOCKET NUMBER: 2026-4063
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4
; TYPE: Amino Acid
; STRANDEDNESS: Single
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide/Protein
; FEATURE:
; OTHER INFORMATION: Mutant 6
US-08-021-608D-22

Query Match 76.2%; Score 16; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IPR 4
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Db 2 IPR 4

RESULT 5

US-08-002-202-15
; Sequence 15, Application US/08002202
; Patent No. 5604201
; GENERAL INFORMATION:
; APPLICANT: Thomas, Garry
; APPLICANT: Anderson, Eric D
; APPLICANT: Thomas, Laurel
; APPLICANT: Haylick, Joel S
; TITLE OF INVENTION: Methods and Reagents for Inhibiting
; TITLE OF INVENTION: Furin Endoprotease
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti and Witcoff, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/002,202
; FILING DATE: 08-JAN-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5604201nan, Kevin E
; REGISTRATION NUMBER: 35,30003
; REFERENCE/DOCKET NUMBER: 92,448
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-002-202-15

Query Match 76.2%; Score 16; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IPR 4
|||
Db 2 IPR 4

RESULT 6

US-08-726-160-22
; Sequence 22, Application US/08726160
; Patent No. 5734016
; GENERAL INFORMATION:
; APPLICANT: LEVENS, DAVID L., DUNCAN,
; APPLICANT: ROBERT C., AND AVIGAN, MARK I.
; TITLE OF INVENTION: NOVEL FUSE BINDING
; TITLE OF INVENTION: PROTEIN AND CDNA THEREFOR
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK

```
/ STATE: NEW YORK
/ COUNTRY: USA
/ ZIP: 10154
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: FLOPPY DISK
/ COMPUTER: IBM PC COMPATIBLE
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: WORDPERFECT 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/726,160
/ FILING DATE: 04-OCT-1996
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/021,608
/ FILING DATE: 22-FEB-1993
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: WILLIAM S. FEILER
/ REGISTRATION NUMBER: 26,728
/ REFERENCE/DOCKET NUMBER: 2026-4063US1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 758-4800
/ TELEFAX: (212) 751-6849
/ INFORMATION FOR SEQ ID NO: 22:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 4
/ TYPE: Amino Acid
/ STRANDEDNESS: Single
/ TOPOLOGY: Unknown
/ MOLECULE TYPE: Peptide/Protein
/ FEATURE:
/ OTHER INFORMATION: Mutant 6
/
US-08-726-160-22

Query Match 76.2%; Score 16; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IPR 4
Db 2 IPR 4

RESULT 7
US-08-685-589A-27
; Sequence 27, Application US/08685589A
; Patent No. 5916872
; GENERAL INFORMATION:
; APPLICANT: Chang, Conway
; APPLICANT: Gu, Leo
; APPLICANT: Chen, Jie
; TITLE OF INVENTION: CYCLIC PEPTIDES HAVING BROAD
; TITLE OF INVENTION: SPECTRUM ANTIMICROBIAL ACTIVITY
; NUMBER OF SEQUENCES: 222
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/685,589A
; FILING DATE: 24-JUL-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 8067-026-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; FILING DATE:

/ STATE: NEW YORK
/ COUNTRY: USA
/ ZIP: 10154
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: FLOPPY DISK
/ COMPUTER: IBM PC COMPATIBLE
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: WORDPERFECT 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/726,160
/ FILING DATE: 04-OCT-1996
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/021,608
/ FILING DATE: 22-FEB-1993
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: WILLIAM S. FEILER
/ REGISTRATION NUMBER: 26,728
/ REFERENCE/DOCKET NUMBER: 2026-4063US1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 758-4800
/ TELEFAX: (212) 751-6849
/ INFORMATION FOR SEQ ID NO: 22:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 4
/ TYPE: Amino Acid
/ STRANDEDNESS: Single
/ TOPOLOGY: Unknown
/ MOLECULE TYPE: Peptide/Protein
/ FEATURE:
/ OTHER INFORMATION: Mutant 6
/
US-08-726-160-22

Query Match 76.2%; Score 16; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIP 3
Db 1 RIP 3

RESULT 8
US-08-685-589A-28
; Sequence 28, Application US/08685589A
; Patent No. 5916872
; GENERAL INFORMATION:
; APPLICANT: Chang, Conway
; APPLICANT: Gu, Leo
; APPLICANT: Chen, Jie
; TITLE OF INVENTION: CYCLIC PEPTIDES HAVING BROAD
; TITLE OF INVENTION: SPECTRUM ANTIMICROBIAL ACTIVITY
; NUMBER OF SEQUENCES: 222
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/685,589A
; FILING DATE: 24-JUL-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 8067-026-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; FILING DATE:
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; TOPOLOGY: No. 5916872 Relevant
; MOLECULE TYPE: Peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..4
; OTHER INFORMATION: /product= "Beta-turn"
US-08-685-589A-28

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Best Local Similarity 100.0%; Pred. No. 4.1e+05;
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Db 1 RIP 3

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; Sequence 29, Application US/08685589A
; Patent No. 5916872
; GENERAL INFORMATION:
; APPLICANT: Chang, Conway
; APPLICANT: Gu, Leo
; APPLICANT: Chen, Jie
; TITLE OF INVENTION: CYCLIC PEPTIDES HAVING BROAD
; TITLE OF INVENTION: SPECTRUM ANTIMICROBIAL ACTIVITY
; NUMBER OF SEQUENCES: 222
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/685,589A
; FILING DATE: 24-JUL-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 8067-026-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: No. 5916872 Relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..4
; OTHER INFORMATION: /product= "Beta-turn"

US-08-685-589A-29
Query Match 76.2%; Score 16; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIP 3

Db 1 RIP 3

RESULT 10
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; Patent No. 6271011
; GENERAL INFORMATION:
; APPLICANT: Lee, Margie
; APPLICANT: Sanchez, Susan
; APPLICANT: Henk, Adam
; TITLE OF INVENTION: Pasteurella Neuraminidase Coding Sequences,
; TITLE OF INVENTION: Compositions and Diagnostic Methods
; FILE REFERENCE: 77-96B
; CURRENT APPLICATION NUMBER: US/09/400,208B
; CURRENT FILING DATE: 1999-09-21
; PRIOR APPLICATION NUMBER: US 08/951,984
; PRIOR FILING DATE: 1997-10-15
; PRIOR APPLICATION NUMBER: US 60/028,876
; PRIOR FILING DATE: 1996-10-16
; PRIOR APPLICATION NUMBER: US 60/028,482
; PRIOR FILING DATE: 1996-10-15
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:oligopeptide
; OTHER INFORMATION: sequence
US-09-400-208B-8

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Best Local Similarity 100.0%; Pred. No. 4.1e+05;
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; Sequence 12, Application US/09400208B
; Patent No. 6271011
; GENERAL INFORMATION:
; APPLICANT: Lee, Margie
; APPLICANT: Sanchez, Susan
; APPLICANT: Henk, Adam
; TITLE OF INVENTION: Pasteurella Neuraminidase Coding Sequences,
; TITLE OF INVENTION: Compositions and Diagnostic Methods
; FILE REFERENCE: 77-96B
; CURRENT APPLICATION NUMBER: US/09/400,208B
; CURRENT FILING DATE: 1999-09-21
; PRIOR APPLICATION NUMBER: US 08/951,984
; PRIOR FILING DATE: 1997-10-15
; PRIOR APPLICATION NUMBER: US 60/028,876
; PRIOR FILING DATE: 1996-10-16
; PRIOR APPLICATION NUMBER: US 60/028,482
; PRIOR FILING DATE: 1996-10-15
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 4
; TYPE: PRT
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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide motif
; OTHER INFORMATION: in Pasteurella multocida neuraminidase
US-09-400-208B-12

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Best Local Similarity 100.0%; Pred. No. 4.1e+05;
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Db |||
2 RIP 4

RESULT 12

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; Sequence 88, Application US/09417608A
; Patent No. 6686164
; GENERAL INFORMATION:
; APPLICANT: Olsen, Arne
; APPLICANT: Roggen, Erwin
; APPLICANT: Ernst, Steffen
; TITLE OF INVENTION: Low Allergenic Protein Variants
; FILE REFERENCE: 5676.200-US
; CURRENT APPLICATION NUMBER: US/09/417,608A
; CURRENT FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn version 3.2
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; ORGANISM: Artificial
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; OTHER INFORMATION: Synthetic
US-09-417-608A-88

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1 R1PR 4

RESULT 13

US-09-400-122A-8
; Sequence 8, Application US/09400122A
; Patent No. 6767713
; GENERAL INFORMATION:
; APPLICANT: Lee, Margie
; APPLICANT: Sanchez, Susan
; APPLICANT: Henk, Adam
; TITLE OF INVENTION: Pasteurella Neuraaminidase Coding Sequences,
; FILE REFERENCE: 77-96A
; CURRENT APPLICATION NUMBER: US/09/400,122A
; CURRENT FILING DATE: 1999-09-21
; PRIOR APPLICATION NUMBER: US 08/951,984
; PRIOR FILING DATE: 1997-10-15
; PRIOR APPLICATION NUMBER: US 60/028,876
; PRIOR FILING DATE: 1996-10-16
; PRIOR APPLICATION NUMBER: US 60/028,482
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; SOFTWARE: PatentIn Ver. 2.0
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; ORGANISM: Artificial Sequence
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US-09-400-122A-8

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Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 14

US-09-400-122A-12
; Sequence 12, Application US/09400122A
; Patent No. 6767713
; GENERAL INFORMATION:
; APPLICANT: Lee, Margie
; APPLICANT: Sanchez, Susan
; APPLICANT: Henk, Adam
; TITLE OF INVENTION: Pasteurella Neuraaminidase Coding Sequences,
; FILE REFERENCE: 77-96A
; CURRENT APPLICATION NUMBER: US/09/400,122A
; CURRENT FILING DATE: 1999-09-21
; PRIOR APPLICATION NUMBER: US 08/951,984
; PRIOR FILING DATE: 1997-10-15
; PRIOR APPLICATION NUMBER: US 60/028,876
; PRIOR FILING DATE: 1996-10-16
; PRIOR APPLICATION NUMBER: US 60/028,482
; PRIOR FILING DATE: 1996-10-15
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: peptide motif
; OTHER INFORMATION: in Pasteurella multocida neuraaminidase
US-09-400-122A-12

Query Match 76.2%; Score 16; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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2 RIP 4

RESULT 15

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; Sequence 1, Application US/08221582A
; Patent No. 5505946
; GENERAL INFORMATION:
; APPLICANT: Ann R. Kennedy, Bernard F. Szuha
; TITLE OF INVENTION: Bowman-Birk Inhibitor Concentrate
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Pre-Malignant Ti
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jane Massey Licata, Esq.
; STREET: 210 Lake Drive East, Suite 201
; CITY: Cherry Hill
; STATE: NJ
; COUNTRY: USA
; ZIP: 08002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM 486
; OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/221,582A
; FILING DATE: April 1, 1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: 07/973,335
; APPLICATION DATE: No. 5505946member 2, 1992
; FILING DATE: No. 5505946member 2, 1992

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; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: UPSC-0027
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 779-8488
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-221-582A-1

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Best Local Similarity 66.7%; Pred. No. 4.1e+05;
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GenCore version 5.1.6
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OM protein - protein search, using sw model

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Title: US-09-885-914B-2

Perfect score: 21

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Searched: 1714042 seqs, 383979560 residues

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Database : Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	16	76.2	4	16 US-10-311-858B-3	Sequence 3, Appli
7	16	76.2	4	16 US-10-311-858B-11	Sequence 11, Appl
8	16	76.2	4	16 US-10-730-454-88	Sequence 88, Appl
9	15	71.4	3	16 US-10-745-733-43	Sequence 43, Appl
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11	15	71.4	4	9 US-09-933-997B-37	Sequence 37, Appl

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13	15	71.4	4	13 US-10-021-963-7	Sequence 7, Appli
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15	15	71.4	4	15 US-10-301-849A-14	Sequence 14, Appl
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17	15	71.4	4	15 US-10-601-953-212	Sequence 212, App
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20	15	71.4	4	16 US-10-311-858B-14	Sequence 14, Appl
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22	14	66.7	3	16 US-10-651-584C-91	Sequence 91, Appl
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41	14	66.7	4	17 US-10-821-240A-235	Sequence 235, App
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59	12	57.1	3	15 US-10-243-613-103	Sequence 103, App
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 100 12 57.1 4 10 US-09-931-009A-2 Sequence 2, Appli

ALIGNMENTS

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 ; Publication No. US20040127396A1
 ; GENERAL INFORMATION:
 ; APPLICANT: DUROIS, Claire
 ; TITLE OF INVENTION: USE OF FURIN AND FURIN-LIKE PROTEASE INHIBITORS IN THE TREATMENT
 ; FILE OF INVENTION: OF INFLAMMATORY OR MATRIX REMODELLING DISEASES
 ; FILE REFERENCE: 85761-28
 ; CURRENT APPLICATION NUMBER: US/09/885,914B
 ; PRIOR FILING DATE: 2001-06-22
 ; PRIOR FILING DATE: 2000-06-26
 ; PRIOR APPLICATION NUMBER: CA 2,312,109
 ; PRIOR FILING DATE: 2000-06-23
 ; NUMBER OF SEQ ID NOS: 3
 ; SOFTWARE: Patentin version 3.2
 ; SEQ ID NO 2
 ; LENGTH: 4
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Variant of Homo sapiens alphan-antitrypsin reactive site
 ; FEATURE:
 ; NAME/KEY: MUTAGEN
 ; LOCATION: (1)..(1)
 ; OTHER INFORMATION: Ala355 to Arg355 variant of reactive site of alphan-antitrypsin
 ; FEATURE:
 ; NAME/KEY: MUTAGEN
 ; LOCATION: (4)..(4)
 ; OTHER INFORMATION: Met358 to Arg358 variant of reactive site of alphan-antitrypsin
 ; US-09-885-914B-2

Query Match 100.0%; Score 21; DB 11; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.5e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 1 RIPR 4

RESULT 2
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 ; Sequence 8, Application US/09400122
 ; Publication No. US20040072153A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lee, Margie
 ; APPLICANT: Sanchez, Susan
 ; APPLICANT: Henk, Adam
 ; TITLE OF INVENTION: Pasteurella Neuraminidase Coding Sequences,
 ; TITLE OF INVENTION: Compositions and Diagnostic Methods

; FILE REFERENCE: 77-96a
 ; CURRENT APPLICATION NUMBER: US/09/400,122
 ; CURRENT FILING DATE: 1999-09-21
 ; EARLIER APPLICATION NUMBER: US 08/951,984
 ; EARLIER FILING DATE: 1997-10-15
 ; EARLIER APPLICATION NUMBER: USV 60/028,876
 ; EARLIER FILING DATE: 1996-10-16
 ; EARLIER APPLICATION NUMBER: US 60/028,482
 ; EARLIER FILING DATE: 1996-10-15
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 8
 ; LENGTH: 4
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:oligopeptide
 ; OTHER INFORMATION: sequence
 ; US-09-400-122-8

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 DB 2 RIP 4

RESULT 3
 US-10-462-452-4
 ; Sequence 4, Application US/10462452
 ; Publication No. US20040037809A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Quay, Steven
 ; APPLICANT: El Shafy, Mohammed Abd
 ; APPLICANT: Gupta, Malini
 ; APPLICANT: de Meireles, Jorge
 ; TITLE OF INVENTION: Compositions and Methods for Enhanced
 ; TITLE OF INVENTION: Mucosal-Delivery of Interferon Beta
 ; FILE REFERENCE: 02-02US
 ; CURRENT APPLICATION NUMBER: US/10/462,452
 ; CURRENT FILING DATE: 2003-06-16
 ; PRIOR APPLICATION NUMBER: 60/393,066
 ; PRIOR FILING DATE: 2002-06-28
 ; NUMBER OF SEQ ID NOS: 790
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 4
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-462-452-4

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 DB 2 RIP 4

RESULT 4
 US-10-601-953-4
 ; Sequence 4, Application US/10601953
 ; Publication No. US20040077540A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Quay, Steven C.
 ; TITLE OF INVENTION: Compositions And Methods For Modulating Physiology Of Epithelial
 ; TITLE OF INVENTION: Junctional Adhesion Molecules For Enhanced Mucosal Delivery Of
 ; TITLE OF INVENTION: Therapeutic Compounds
 ; FILE REFERENCE: 02-03US
 ; CURRENT APPLICATION NUMBER: US/10/601,953

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; CURRENT FILING DATE: 2003-06-24
; PRIOR APPLICATION NUMBER: 60/392,512
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 900
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-601-953-4

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Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIP 3
Db 2 RIP 4

RESULT 5
US-10-322-266-4
; Sequence 4, Application US/10322266
; Publication No. US20040115135A1
; GENERAL INFORMATION:
; APPLICANT: Quay, Steven C.
; TITLE OF INVENTION: Compositions And Methods For Enhanced Mucosal Delivery Of Peptide
; FILE REFERENCE: NPCI0567
; CURRENT APPLICATION NUMBER: US/10/322,266
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 797
; SOFTWARE: PatentIn version 3.2
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; ORGANISM: Artificial Sequence
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US-10-322-266-4

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QY 1 RIP 3
Db 2 RIP 4

RESULT 6
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; Publication No. US20040116656A1
; GENERAL INFORMATION:
; APPLICANT: DU, Yucang
; APPLICANT: SHEN, Jinhuan
; TITLE OF INVENTION: A Kind of Memory-enhancing Peptides and Their Application
; FILE REFERENCE: SHA 110
; CURRENT APPLICATION NUMBER: US/10/311,858B
; CURRENT FILING DATE: 2003-08-25
; PRIOR APPLICATION NUMBER: PCT/CN01/00875
; PRIOR FILING DATE: 2001-05-28
; NUMBER OF SEQ ID NOS: 16
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Fragments
US-10-311-858B-3

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QY 1 RIP 3
Db 2 RIP 4

RESULT 7
US-10-311-858B-11
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; Publication No. US20040116656A1
; GENERAL INFORMATION:
; APPLICANT: DU, Yucang
; APPLICANT: SHEN, Jinhuan
; TITLE OF INVENTION: A Kind of Memory-enhancing Peptides and Their Application
; FILE REFERENCE: SHA 110
; CURRENT APPLICATION NUMBER: US/10/311,858B
; CURRENT FILING DATE: 2003-08-25
; PRIOR APPLICATION NUMBER: PCT/CN01/00875
; PRIOR FILING DATE: 2001-05-28
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US-10-311-858B-11

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QY 2 IPR 4
Db 2 IPR 4

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; Publication No. US20040175757A1
; GENERAL INFORMATION:
; APPLICANT: Olsen, Arne
; APPLICANT: Roggen, Erwin
; APPLICANT: Ernst, Steffen
; TITLE OF INVENTION: Low Allergenic Protein Variants
; FILE REFERENCE: 5676.200-US
; CURRENT APPLICATION NUMBER: US/10/730,454
; CURRENT FILING DATE: 2003-12-08
; PRIOR APPLICATION NUMBER: US/09/417,608
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 88
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-730-454-88

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; Publication No. US20040259113A1
; GENERAL INFORMATION:
; APPLICANT: Tindall, D.J.
; APPLICANT: Young, C.Y.F.
; APPLICANT: McCormick, D.J.
; APPLICANT: Klee, G.G.
; APPLICANT: Saedi, M.S.
; APPLICANT: Kumar, A.
; APPLICANT: Rittenhouse, H.G.
; APPLICANT: Wolfert, R.L.
; TITLE OF INVENTION: Method for detection of metastatic prostate cancer
; FILE REFERENCE: 545.005U1
; CURRENT APPLICATION NUMBER: US/10/745,733
; CURRENT FILING DATE: 2003-12-23
; PRIOR APPLICATION NUMBER: US/08/759,354
; PRIOR FILING DATE: 1996-11-14
; PRIOR APPLICATION NUMBER: PCT/US96/06167
; PRIOR FILING DATE: 1996-05-02
; PRIOR APPLICATION NUMBER: US 08/622,046
; PRIOR FILING DATE: 1996-03-26
; PRIOR APPLICATION NUMBER: US 08/427,767
; PRIOR FILING DATE: 1995-05-02
; PRIOR APPLICATION NUMBER: US 08/241,174
; PRIOR FILING DATE: 1994-05-10
; PRIOR APPLICATION NUMBER: US 08/096,946
; PRIOR FILING DATE: 1993-07-22
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
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; LENGTH: 3
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-745-733-43

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Db      1 RVP 3

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; Publication No. US20020039748A1
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Foster, Donald C.
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: KUNITZ DOMAIN POLYPEPTIDE AND MATERIALS
; FILE REFERENCE: 98-22
; CURRENT APPLICATION NUMBER: US/09/778,885
; CURRENT FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 09/320,095
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: US 60/087,032
; PRIOR FILING DATE: 1998-05-28
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; FEATURE:
; OTHER INFORMATION: thrombin cleavage site
US-09-778-885-11

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Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RIP 3
Db      1 RVP 3

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; Patent No. US20020098193A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Elizabeth S.
; TITLE OF INVENTION: IMMUGLOBIN-LIKE DOMAINS WITH INCREASED HALF LIVES
; FILE REFERENCE: UTSD:483
; CURRENT APPLICATION NUMBER: US/09/933,497B
; CURRENT FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 60/013,563
; PRIOR FILING DATE: 1996-03-18
; NUMBER OF SEQ ID NOS: 39
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QY      2 IPR 4
Db      2 VPR 4

RESULT 12
US-09-819-136-6
; Sequence 6, Application US/09819136
; Patent No. US20020146789A1
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: MULTI-DOMAIN PROTEINASE INHIBITOR
; FILE REFERENCE: 00-25
; CURRENT APPLICATION NUMBER: US/09/819,136
; CURRENT FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/193,642
; PRIOR FILING DATE: 2000-03-31
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; ORGANISM: Artificial Sequence
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; OTHER INFORMATION: thrombin cleavage site
US-09-819-136-6

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QY      2 IPR 4
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RESULT 13
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; Sequence 7, Application US/10021963
; Publication No. US20020110887A1
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell C.
; TITLE OF INVENTION: KUNITZ DOMAIN POLYPEPTIDE ZKUNG
; FILE REFERENCE: 98-40
; CURRENT APPLICATION NUMBER: US/10/021,963
; CURRENT FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US/09/388,183
; PRIOR FILING DATE: 1999-09-01
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; SOFTWARE: Fast-Seq for Windows Version 3.0
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US-10-021-963-7

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; GENERAL INFORMATION:
; APPLICANT: Quay, Steven
; APPLICANT: El Shafy, Mohammed Abd
; APPLICANT: Gupta, Malini
; APPLICANT: de Melreles, Jorge
; TITLE OF INVENTION: Compositions and Methods for Enhanced
; TITLE OF INVENTION: Mucosal-Delivery of Interferon Beta
; FILE REFERENCE: 02-02US
; CURRENT APPLICATION NUMBER: US/10/462,452
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/393,066
; PRIOR FILING DATE: 2002-06-28
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; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 130
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-462-452-130

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Db      2 RVP 4

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; Sequence 14, Application US/10301849A
; Publication No. US20040040053A1
; GENERAL INFORMATION:
; APPLICANT: Goshima, Naoki
; APPLICANT: Kisu, Yasutomo
; APPLICANT: Sono, Saki
; TITLE OF INVENTION: Method For the Preparation of Nucleic Acids
; FILE REFERENCE: 0942.5600000
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2	21	100.0	4	17	US-09-372-003-15	Sequence 15, Appl
3	21	100.0	4	23	US-09-885-914B-2	Sequence 2, Appl
4	16	76.2	4	1	PCT-US03-19261-4	Sequence 4, Appl
5	16	76.2	4	1	PCT-US03-19994-4	Sequence 27, Appl
6	16	76.2	4	1	PCT-US97-12974A-27	Sequence 27, Appl
7	16	76.2	4	1	PCT-US97-12974A-28	Sequence 28, Appl
8	16	76.2	4	1	PCT-US97-12974A-29	Sequence 29, Appl
9	16	76.2	4	1	PCT-US97-19557-27	Sequence 27, Appl
10	16	76.2	4	1	PCT-US97-19557-28	Sequence 28, Appl
11	16	76.2	4	1	PCT-US97-19557-29	Sequence 29, Appl
12	16	76.2	4	3	US-07-929-181B-20	Sequence 20, Appl
13	16	76.2	4	13	US-08-951-984-8	Sequence 8, Appl
14	16	76.2	4	16	US-09-290-034C-3	Sequence 3, Appl
15	16	76.2	4	16	US-09-290-034C-5	Sequence 5, Appl
16	16	76.2	4	17	US-09-340-852-27	Sequence 27, Appl
17	16	76.2	4	17	US-09-340-852-28	Sequence 28, Appl
18	16	76.2	4	17	US-09-340-852-29	Sequence 29, Appl
19	16	76.2	4	29	US-10-311-858B-3	Sequence 3, Appl
20	16	76.2	4	29	US-10-311-858B-11	Sequence 11, Appl
21	16	76.2	4	29	US-10-322-266-4	Sequence 4, Appl
22	16	76.2	4	30	US-10-462-452-4	Sequence 4, Appl
23	16	76.2	4	32	US-10-601-953-4	Sequence 4, Appl
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59	15	71.4	4	32	US-10-633-690-87	Sequence 87, Appl
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SEQUENCE 246, App
SEQUENCE 247, App
SEQUENCE 248, App
SEQUENCE 249, App
SEQUENCE 37, Appl
SEQUENCE 58, Appl
SEQUENCE 200, App
SEQUENCE 201, App
SEQUENCE 202, App
SEQUENCE 203, App
SEQUENCE 58, Appl
SEQUENCE 200, App
SEQUENCE 201, App
SEQUENCE 202, App
SEQUENCE 203, App
SEQUENCE 58, Appl
SEQUENCE 200, App
SEQUENCE 201, App
SEQUENCE 202, App
SEQUENCE 203, App
SEQUENCE 12, Appl
SEQUENCE 33, Appl
SEQUENCE 1, Appl
SEQUENCE 12, Appl

US-09-372-003-10
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
Query Match 100.0%; Score 21; DB 17; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIPR 4
DB 1 RIPR 4

RESULT 2
US-09-372-003-15
SEQUENCE 15, Application US/09372003
GENERAL INFORMATION:
APPLICANT: Thomas, Gary
APPLICANT: Anderson, Eric D
APPLICANT: Thomas, Laurel
APPLICANT: Hayflick, Joel S
APPLICANT: Nelson, Jay
APPLICANT: Stenglen, Stephan G
TITLE OF INVENTION: Methods and Reagents for Inhibiting Furin
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESS: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/372,003
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/481,534
FILING DATE: 14-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Noonan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 92,448-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
TELEX:
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-372-003-15
Query Match 100.0%; Score 21; DB 17; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIPR 4
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Db 1 R1P 4
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RESULT 3

PCT-US03-19261-4
; Sequence 4: Application PC/TUS0319261
; GENERAL INFORMATION:
; APPLICANT: Quay, Steven
; TITLE OF INVENTION: USE OF FURIN AND FURIN-LIKE PROTEASE INHIBITORS IN THE TREATMENT
; TITLE OF INVENTION: OF INFLAMMATORY OR MATRIX REMODELLING DISEASES
; FILE REFERENCE: 85761-28
; CURRENT APPLICATION NUMBER: US/09/885,914B
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/213,995
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: CA 2,312,109
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Homo sapiens alphas-antitrypsin reactive site
; NAME/KEY: MUTAGEN
; LOCATION: (1)..(1)
; OTHER INFORMATION: Ala355 to Arg355 variant of reactive site of alphas-antitrypsin
; FEATURE:
; NAME/KEY: MUTAGEN
; LOCATION: (4)..(4)
; OTHER INFORMATION: Met358 to Arg358 variant of reactive site of alphas-antitrypsin
US-09-885-914B-2

Query Match 100.0%; Score 21; DB 23; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 R1P 4
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Db 1 R1P 4

RESULT 4

PCT-US03-19261-4
; Sequence 4: Application PC/TUS0319261
; GENERAL INFORMATION:
; APPLICANT: Quay, Steven
; APPLICANT: El Shafy, Mohammed Abd
; APPLICANT: Gupta, Malini
; APPLICANT: de Meireles, Jorge
; TITLE OF INVENTION: Compositions and Methods for Enhanced
; TITLE OF INVENTION: Mucosal-Delivery of Interferon Beta
; FILE REFERENCE: 02-02PCT
; CURRENT APPLICATION NUMBER: PCT/US03/19261
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: 60/393,066
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 790
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-19261-4

Query Match 76.2%; Score 16; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 R1P 3

Db 2 R1P 4
||||

RESULT 5

PCT-US03-19994-4
; Sequence 4: Application PC/TUS0319994
; GENERAL INFORMATION:
; APPLICANT: Quay, Steven C.
; TITLE OF INVENTION: Compositions And Methods For Modulating Physiology Of Epithelial
; TITLE OF INVENTION: Junctional Adhesion Molecules For Enhanced Mucosal Delivery Of
; FILE REFERENCE: 02-03PCT
; CURRENT APPLICATION NUMBER: PCT/US03/19994
; CURRENT FILING DATE: 2003-06-24
; PRIOR APPLICATION NUMBER: 60/392,512
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 900
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
PCT-US03-19994-4

Query Match 76.2%; Score 16; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 R1P 3
||||

Db 2 R1P 4

RESULT 6

PCT-US97-12974A-27
; Sequence 27: Application PC/TUS9712974A
; GENERAL INFORMATION:
; APPLICANT: Chang, Conway
; APPLICANT: Gu, Leo
; APPLICANT: Chen, Jie
; TITLE OF INVENTION: CYCLIC PEPTIDES HAVING BROAD
; TITLE OF INVENTION: SPECTRUM ANTIMICROBIAL ACTIVITY
; NUMBER OF SEQUENCES: 241
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/12974A
; FILING DATE: 23 Jul 97
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/685,589
; FILING DATE: 24-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 8067-026-228
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141

Query	1	RIP	3	Best Local Similarity	100.0%;	Pred. No. 6.4e+06;	Mismatches	0;	Indels	0;	Gaps	0;
Db	1	RIP	3	Best Local Similarity	100.0%;	Pred. No. 6.4e+06;	Mismatches	0;	Indels	0;	Gaps	0;
<p>INFORMATION FOR SEQ ID NO: 27:</p> <p>SEQUENCE CHARACTERISTICS:</p> <p>LENGTH: 4 amino acids</p> <p>TYPE: amino acid</p> <p>STRANDEDNESS: unknown</p> <p>TOPOLOGY: not relevant</p> <p>MOLECULE TYPE: peptide</p> <p>FEATURE:</p> <p>NAME/KEY: Peptide</p> <p>LOCATION: 1..4</p> <p>OTHER INFORMATION: /product= "Beta-turn"</p> <p>PCT-US97-12974A-27</p> <p>Query Match 76.2%; Score 16; DB 1; Length 4;</p> <p>Best Local Similarity 100.0%; Pred. No. 6.4e+06;</p> <p>Mismatches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p> <p>Qy 1 RIP 3</p> <p>Db 1 RIP 3</p> <p>RESULT 8</p> <p>PCT-US97-12974A-29</p> <p>Sequence 29, Application PC/TUS9712974A</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Chang, Conway</p> <p>APPLICANT: Gu, Leo</p> <p>APPLICANT: Chen, Jie</p> <p>TITLE OF INVENTION: CYCLIC PEPTIDES HAVING BROAD</p> <p>TITLE OF INVENTION: SPECTRUM ANTIMICROBIAL ACTIVITY</p> <p>NUMBER OF SEQUENCES: 241</p> <p>CORRESPONDENCE ADDRESS:</p> <p>ADDRESSEE: Pennie & Edmonds LLP</p> <p>STREET: 1155 Avenue of the Americas</p> <p>CITY: New York</p> <p>STATE: New York</p> <p>COUNTRY: USA</p> <p>ZIP: 10036</p> <p>COMPUTER READABLE FORM:</p> <p>MEDIUM TYPE: Floppy disk</p> <p>COMPUTER: IBM PC compatible</p> <p>OPERATING SYSTEM: PC-DOS/MS-DOS</p> <p>SOFTWARE: PatentIn Release #1.0, Version #1.30</p> <p>CURRENT APPLICATION DATA:</p> <p>APPLICATION NUMBER: PCT/US97/12974A</p> <p>FILING DATE: 23 Jul 97</p> <p>CLASSIFICATION:</p> <p>PRIOR APPLICATION DATA:</p> <p>APPLICATION NUMBER: US 08/685,589</p> <p>FILING DATE: 24-JUL-1996</p> <p>ATTORNEY/AGENT INFORMATION:</p> <p>NAME: Coruzzi, Laura A.</p> <p>REGISTRATION NUMBER: 30,742</p> <p>REFERENCE/DOCKET NUMBER: 8067-026-228</p> <p>TELEPHONE: 212-790-9090</p> <p>TELEFAX: 212-869-9741</p> <p>TELEX: 66141</p> <p>INFORMATION FOR SEQ ID NO: 29:</p> <p>SEQUENCE CHARACTERISTICS:</p> <p>LENGTH: 4 amino acids</p> <p>TYPE: amino acid</p> <p>STRANDEDNESS: unknown</p> <p>TOPOLOGY: not relevant</p> <p>MOLECULE TYPE: peptide</p> <p>FEATURE:</p> <p>NAME/KEY: Peptide</p> <p>LOCATION: 1..4</p> <p>OTHER INFORMATION: /product= "Beta-turn"</p> <p>PCT-US97-12974A-29</p> <p>Query Match 76.2%; Score 16; DB 1; Length 4;</p> <p>Best Local Similarity 100.0%; Pred. No. 6.4e+06;</p> <p>Mismatches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p> <p>Qy 1 RIP 3</p> <p>Db 1 RIP 3</p> <p>RESULT 9</p> <p>PCT-US97-12974A-27</p> <p>Sequence 27, Application PC/TUS9719557</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Chang, Conway</p> <p>APPLICANT: Gu, Leo</p>												


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; LOCATION: 1..4
; OTHER INFORMATION: /product= "Beta-turn"
PCT-US97-19557-29

Query Match          76.2%; Score 16; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIP 3
DB 1 RIP 3

RESULT 12
US-07-929-181B-20
; Sequence 20, Application US/07929181B
; GENERAL INFORMATION:
; APPLICANT: Rath, Matthias
; TITLE OF INVENTION: TETRAPEPTIDE AND METHOD OF USE
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SHELDON & MAK
; STREET: 401 Florence Street, First Floor
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk, 3.50 inch, 1.44 MB
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/929,181B
; FILING DATE: 07-AUG-1992
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Cranfill, Raymond B
; REGISTRATION NUMBER: 32,845
; REFERENCE/DOCKET NUMBER: RATH-10007.00
; TELEPHONE: 415-322-5333
; TELEFAX: 415-322-5499
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-07-929-181B-20

Query Match          76.2%; Score 16; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IPR 4
DB 2 IPR 4

RESULT 13
US-08-951-984-8
; Sequence 8, Application US/08951984
; GENERAL INFORMATION:
; APPLICANT: Lee, Margie
; APPLICANT: Henk, Adam
; TITLE OF INVENTION: Neutaminidase, Coding Sequences,
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder

Query Match          76.2%; Score 16; DB 16; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IPR 4
DB 2 IPR 4

; LOCATION: Colorado
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/951,984
; FILING DATE: 15-OCT-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/028,482
; FILING DATE: 15-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/028,876
; FILING DATE: 16-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferber, Donna M.
; REGISTRATION NUMBER: 33,878
; REFERENCE/DOCKET NUMBER: 77-96
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
US-08-951-984-8

Query Match          76.2%; Score 16; DB 13; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIP 3
DB 2 RIP 4

RESULT 14
US-09-290-034C-3
; Sequence 3, Application US/09290034C
; GENERAL INFORMATION:
; APPLICANT: Jean, Francois
; APPLICANT: Thomas, Gary
; TITLE OF INVENTION: Reagents and Methods for Inhibiting Furin Endoprotease
; FILE REFERENCE: 92448-H
; CURRENT APPLICATION NUMBER: US/09/290,034C
; CURRENT FILING DATE: 1999-04-08
; PRIOR APPLICATION NUMBER: 60/081,034
; PRIOR FILING DATE: 1998-04-09
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: elastase
; OTHER INFORMATION: recognition site
US-09-290-034C-3

Query Match          76.2%; Score 16; DB 16; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IPR 4
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Db |||
2 IPR 4

RESULT 15
US-09-290-034C-5
; Sequence 5: Application US/09290034C
; GENERAL INFORMATION:
; APPLICANT: Jean, Francois
; TITLE OF INVENTION: Reagents and Methods for Inhibiting Furin Endoprotease
; FILE REFERENCE: 92448-H
; CURRENT APPLICATION NUMBER: US/09/290,034C
; CURRENT FILING DATE: 1999-04-08
; PRIOR APPLICATION NUMBER: 60/081,034
; PRIOR FILING DATE: 1998-04-09
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: furin
; OTHER INFORMATION: recognition sequence
; NAME/KEY: SITE
; LOCATION: (2)
; OTHER INFORMATION: Xaa residue can be any amino acid
US-09-290-034C-5

Query Match 76.2%; Score 16; DB 16; Length 4;
Best Local Similarity 75.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPR 4
|||
Db 1 RXPR 4

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Job time : 330.5 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2005, 16:30:17 ; Search time 37 Seconds
(without alignments)
13.327 Million cell updates/sec

Title: US-09-885-914B-2

Perfect score: 21

Sequence: 1 R1P4 4

Scoring table: BLOSUM62

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Searched: 583429 seqs, 123271311 residues

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Pending Patents AA New:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	17	81.0	4	6	US-10-892-402-144
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5	15	71.4	3	6	US-10-529-163-30
6	15	71.4	4	6	US-10-892-402-11
7	15	71.4	4	6	US-10-892-402-59
8	15	71.4	4	6	US-10-892-402-100
9	15	71.4	4	6	US-10-892-402-104
10	15	71.4	4	6	US-10-123-036B-17
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16	14	66.7	4	6	US-10-498-691A-16
17	13	61.9	3	7	US-11-138-966-679
18	13	61.9	4	6	US-10-924-367A-3
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20	12	57.1	3	6	US-10-490-776A-331
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22	12	57.1	3	7	US-11-066-697-1153
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24	12	57.1	4	5	US-09-868-813B-6
25	12	57.1	4	6	US-10-467-657A-6678

26	12	57.1	4	6	US-10-524-157-1	Sequence 1, Appli
27	12	57.1	4	6	US-10-356-656-10	Sequence 10, Appl
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45	12	57.1	4	6	US-10-892-402-152	Sequence 152, App
46	12	57.1	4	6	US-10-529-115-1	Sequence 1, Appli
47	12	57.1	4	6	US-10-467-657A-6678	Sequence 6678, Ap
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51	12	57.1	4	6	US-10-684-796-512	Sequence 512, App
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53	12	57.1	4	6	US-10-857-484-74	Sequence 74, Appl
54	12	57.1	4	7	US-11-030-232-341	Sequence 341, App
55	12	57.1	4	7	US-11-030-232-342	Sequence 342, App
56	12	57.1	4	7	US-11-030-232-344	Sequence 344, App
57	12	57.1	4	7	US-11-030-232-345	Sequence 345, App
58	12	57.1	4	7	US-11-030-232-347	Sequence 347, App
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60	12	57.1	4	7	US-11-038-326-11	Sequence 11, Appl
61	12	57.1	4	7	US-11-038-326-13	Sequence 13, Appl
62	12	57.1	4	7	US-11-051-267-23	Sequence 23, Appl
63	12	57.1	4	7	US-11-065-669-25	Sequence 25, Appl
64	12	57.1	4	7	US-11-066-697-1539	Sequence 1539, Ap
65	12	57.1	4	7	US-11-066-697-1553	Sequence 1553, Ap
66	12	57.1	4	7	US-11-066-697-1558	Sequence 1558, Ap
67	12	57.1	4	7	US-11-066-697-1563	Sequence 1563, Ap
68	12	57.1	4	7	US-11-080-973-25	Sequence 25, Appl
69	12	57.1	4	7	US-11-129-741-3986	Sequence 3986, Ap
70	11	52.4	2	1	PCT-IL05-00211-451	Sequence 451, App
71	11	52.4	2	1	PCT-IL05-00211-1047	Sequence 1047, Ap
72	11	52.4	2	1	PCT-IL05-00211-1365	Sequence 1365, Ap
73	11	52.4	2	1	PCT-IL05-00211-1526	Sequence 1526, Ap
74	11	52.4	2	1	PCT-IL05-00211-1537	Sequence 1537, Ap
75	11	52.4	3	1	PCT-IL05-00211-484	Sequence 484, App
76	11	52.4	3	1	PCT-IL05-00211-485	Sequence 485, App
77	11	52.4	3	1	PCT-IL05-00211-1071	Sequence 1071, Ap
78	11	52.4	3	1	PCT-IL05-00211-1072	Sequence 1072, Ap
79	11	52.4	3	1	PCT-IL05-00211-1382	Sequence 1382, Ap
80	11	52.4	3	1	PCT-IL05-00211-1383	Sequence 1383, Ap
81	11	52.4	3	1	PCT-IL05-00211-1588	Sequence 1588, Ap
82	11	52.4	3	1	PCT-IL05-00211-1589	Sequence 1589, Ap
83	11	52.4	3	1	PCT-IL05-00211-1599	Sequence 1599, Ap
84	11	52.4	3	1	PCT-IL05-00211-1600	Sequence 1600, Ap
85	11	52.4	4	1	PCT-US05-08075-26	Sequence 26, Appl
86	11	52.4	4	1	PCT-IL05-00211-516	Sequence 516, App
87	11	52.4	4	1	PCT-IL05-00211-517	Sequence 517, App
88	11	52.4	4	1	PCT-IL05-00211-518	Sequence 518, App
89	11	52.4	4	1	PCT-IL05-00211-1094	Sequence 1094, Ap
90	11	52.4	4	1	PCT-IL05-00211-1095	Sequence 1095, Ap
91	11	52.4	4	1	PCT-IL05-00211-1096	Sequence 1096, Ap
92	11	52.4	4	1	PCT-IL05-00211-1398	Sequence 1398, Ap
93	11	52.4	4	1	PCT-IL05-00211-1399	Sequence 1399, Ap
94	11	52.4	4	1	PCT-IL05-00211-1400	Sequence 1400, Ap
95	11	52.4	4	1	PCT-IL05-00211-1649	Sequence 1649, Ap
96	11	52.4	4	1	PCT-IL05-00211-1650	Sequence 1650, Ap
97	11	52.4	4	1	PCT-IL05-00211-1651	Sequence 1651, Ap
98	11	52.4	4	1	PCT-IL05-00211-1660	Sequence 1660, Ap

Sequence 1661, Ap
Sequence 1662, Ap

99 11 52.4 4 1 PCT-IL05-00211-1661
100 11 52.4 4 1 PCT-IL05-00211-1662

ALIGNMENTS

RESULT 1
US-10-892-402-108
; Sequence 108, Application US/10892402
; GENERAL INFORMATION:
; APPLICANT: Harris, Jennifer L.
; APPLICANT: Damoiseaux, Robert
; APPLICANT: Backes, Bradley J.
; APPLICANT: Winssinger, Nicolas
; APPLICANT: IRM LLC
; TITLE OF INVENTION: Fluorogenic Enzyme Substrates and Uses
; FILE REFERENCE: 021288-000410US
; CURRENT APPLICATION NUMBER: US/10/892,402
; PRIOR FILING DATE: 2004-07-14
; PRIOR APPLICATION NUMBER: US 60/487,464
; PRIOR FILING DATE: 2003-07-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 108
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: rhodamine protease substrate library peptide
US-10-892-402-108

Query Match 95.2%; Score 20; DB 6; Length 4;
Best Local Similarity 75.0%; Pred. No. 5.4e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 R1PR 4
|:|
Db 1 RVPR 4

RESULT 2
US-10-892-402-144
; Sequence 144, Application US/10892402
; GENERAL INFORMATION:
; APPLICANT: Harris, Jennifer L.
; APPLICANT: Damoiseaux, Robert
; APPLICANT: Backes, Bradley J.
; APPLICANT: Winssinger, Nicolas
; APPLICANT: IRM LLC
; TITLE OF INVENTION: Fluorogenic Enzyme Substrates and Uses
; FILE REFERENCE: 021288-000410US
; CURRENT APPLICATION NUMBER: US/10/892,402
; PRIOR FILING DATE: 2004-07-14
; PRIOR APPLICATION NUMBER: US 60/487,464
; PRIOR FILING DATE: 2003-07-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 144
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: rhodamine protease substrate library peptide
US-10-892-402-144

Query Match 81.0%; Score 17; DB 6; Length 4;
Best Local Similarity 75.0%; Pred. No. 5.4e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 R1PR 4

Db 1 R1PR 4
|:|

RESULT 3
US-10-892-402-120
; Sequence 120, Application US/10892402
; GENERAL INFORMATION:
; APPLICANT: Harris, Jennifer L.
; APPLICANT: Damoiseaux, Robert
; APPLICANT: Backes, Bradley J.
; APPLICANT: Winssinger, Nicolas
; APPLICANT: IRM LLC
; TITLE OF INVENTION: Fluorogenic Enzyme Substrates and Uses
; FILE REFERENCE: 021288-000410US
; CURRENT APPLICATION NUMBER: US/10/892,402
; PRIOR FILING DATE: 2004-07-14
; PRIOR APPLICATION NUMBER: US 60/487,464
; PRIOR FILING DATE: 2003-07-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 120
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: rhodamine protease substrate library peptide
US-10-892-402-120

Query Match 76.2%; Score 16; DB 6; Length 4;
Best Local Similarity 75.0%; Pred. No. 5.4e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 R1PR 4
|:|
Db 1 R1PR 4

RESULT 4
US-10-529-163-28
; Sequence 28, Application US/10529163
; GENERAL INFORMATION:
; APPLICANT: YOUSEF, et al.
; TITLE OF INVENTION: Methods for Detecting Endocrine Cancer
; FILE REFERENCE: 11757.82USWO
; CURRENT APPLICATION NUMBER: US/10/529,163
; CURRENT FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: US 60/414,107
; PRIOR FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/450,406
; PRIOR FILING DATE: 2003-02-26
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 28
; LENGTH: 3
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Peptide fragment of a Fluorogenic Synthetic Peptide
US-10-529-163-28

Query Match 71.4%; Score 15; DB 6; Length 3;
Best Local Similarity 66.7%; Pred. No. 5.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 IPR 4
|:|
Db 1 VPR 3

RESULT 5
US-10-529-163-30

; Sequence 30, Application US/10529163
; GENERAL INFORMATION:
; APPLICANT: YOUSEF, et al.
; TITLE OF INVENTION: Methods for Detecting Endocrine Cancer
; FILE REFERENCE: 021288-000410US
; CURRENT APPLICATION NUMBER: US/10/529,163
; CURRENT FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: US 60/414,107
; PRIOR FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/450,406
; PRIOR FILING DATE: 2003-02-26
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 30
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Peptide Portion of Trypsin Substrate
US-10-529-163-30

Query Match 71.4%; Score 15; DB 6; Length 3;
Best Local Similarity 66.7%; Pred. No. 5.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 IPR 4
DB 1 VPR 3

RESULT 6
US-10-892-402-11
; Sequence 11, Application US/10892402
; GENERAL INFORMATION:
; APPLICANT: Harris, Jennifer L.
; APPLICANT: Damoiseaux, Robert
; APPLICANT: Backes, Bradley J.
; APPLICANT: Winsinger, Nicolas
; APPLICANT: IRM LLC
; TITLE OF INVENTION: Fluorogenic Enzyme Substrates and Uses
; FILE REFERENCE: 021288-000410US
; CURRENT APPLICATION NUMBER: US/10/892,402
; CURRENT FILING DATE: 2004-07-14
; PRIOR APPLICATION NUMBER: US 60/487,464
; PRIOR FILING DATE: 2003-07-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: rhodamine protease substrate library peptide
US-10-892-402-11

Query Match 71.4%; Score 15; DB 6; Length 4;
Best Local Similarity 66.7%; Pred. No. 5.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 IPR 4
DB 2 VPR 4

RESULT 7
US-10-892-402-59
; Sequence 59, Application US/10892402
; GENERAL INFORMATION:
; APPLICANT: Harris, Jennifer L.
; APPLICANT: Damoiseaux, Robert
; APPLICANT: Backes, Bradley J.
; APPLICANT: Winsinger, Nicolas

; APPLICANT: IRM LLC
; TITLE OF INVENTION: Fluorogenic Enzyme Substrates and Uses
; FILE REFERENCE: 021288-000410US
; CURRENT APPLICATION NUMBER: US/10/892,402
; CURRENT FILING DATE: 2004-07-14
; PRIOR APPLICATION NUMBER: US 60/487,464
; PRIOR FILING DATE: 2003-07-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 59
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: rhodamine protease substrate library peptide
US-10-892-402-59

Query Match 71.4%; Score 15; DB 6; Length 4;
Best Local Similarity 66.7%; Pred. No. 5.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 IPR 4
DB 2 VPR 4

RESULT 8
US-10-892-402-100
; Sequence 100, Application US/10892402
; GENERAL INFORMATION:
; APPLICANT: Harris, Jennifer L.
; APPLICANT: Damoiseaux, Robert
; APPLICANT: Backes, Bradley J.
; APPLICANT: Winsinger, Nicolas
; APPLICANT: IRM LLC
; TITLE OF INVENTION: Fluorogenic Enzyme Substrates and Uses
; FILE REFERENCE: 021288-000410US
; CURRENT APPLICATION NUMBER: US/10/892,402
; CURRENT FILING DATE: 2004-07-14
; PRIOR APPLICATION NUMBER: US 60/487,464
; PRIOR FILING DATE: 2003-07-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 100
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: rhodamine protease substrate library peptide
US-10-892-402-100

Query Match 71.4%; Score 15; DB 6; Length 4;
Best Local Similarity 66.7%; Pred. No. 5.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIP 3
DB 1 RVP 3

RESULT 9
US-10-892-402-104
; Sequence 104, Application US/10892402
; GENERAL INFORMATION:
; APPLICANT: Harris, Jennifer L.
; APPLICANT: Damoiseaux, Robert
; APPLICANT: Backes, Bradley J.
; APPLICANT: Winsinger, Nicolas
; APPLICANT: IRM LLC
; TITLE OF INVENTION: Fluorogenic Enzyme Substrates and Uses
; FILE REFERENCE: 021288-000410US
; CURRENT APPLICATION NUMBER: US/10/892,402
; CURRENT FILING DATE: 2004-07-14
; PRIOR APPLICATION NUMBER: US 60/487,464
; PRIOR FILING DATE: 2003-07-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 104
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: rhodamine protease substrate library peptide
US-10-892-402-104

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; FILE REFERENCE: 021288-000410US
; CURRENT APPLICATION NUMBER: US/10/892,402
; CURRENT FILING DATE: 2004-07-14
; PRIOR APPLICATION NUMBER: US 60/487,464
; PRIOR FILING DATE: 2003-07-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 104
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: rhodamine protease substrate library peptide
US-10-892-402-104

Query Match      71.4%; Score 15; DB 6; Length 4;
Best Local Similarity 66.7%; Pred. No. 5.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RIP 3
      |.|
Db      1 RVP 3

RESULT 10
US-10-123-036B-17
; Sequence 17, Application US/10123036B
; GENERAL INFORMATION:
; APPLICANT: Children's Hospital Research Foundation
; TITLE OF INVENTION: METHODS FOR THE TREATMENT OF HEPATIC DISORDERS
; FILE REFERENCE: 0010872/0483963
; CURRENT APPLICATION NUMBER: US/10/123,036B
; CURRENT FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 60/283,788
; PRIOR FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-123-036B-17

Query Match      71.4%; Score 15; DB 6; Length 4;
Best Local Similarity 66.7%; Pred. No. 5.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 IPR 4
      :||
Db      2 VPR 4

RESULT 11
US-11-106-715-87
; Sequence 87, Application US/11106715
; GENERAL INFORMATION:
; APPLICANT: Byrd, Devon
; APPLICANT: Youg, Alice
; APPLICANT: Hartley, James
; TITLE OF INVENTION: Compositions and Methods for Molecular Biology
; FILE REFERENCE: 0942.5230004
; CURRENT APPLICATION NUMBER: US/11/106,715
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US/10/633,690
; PRIOR FILING DATE: 2003-08-05
; PRIOR APPLICATION NUMBER: US 60/400,704
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: US 60/403,095
; PRIOR FILING DATE: 2002-08-14
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 87
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: thrombin cleavage site
US-11-106-715-87

Query Match      71.4%; Score 15; DB 7; Length 4;
Best Local Similarity 66.7%; Pred. No. 5.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 IPR 4
      :||
Db      2 VPR 4

RESULT 12
US-10-892-402-76
; Sequence 76, Application US/10892402
; GENERAL INFORMATION:
; APPLICANT: Harris, Jennifer L.
; APPLICANT: Damoiseaux, Robert
; APPLICANT: Backes, Bradley J.
; APPLICANT: Winsinger, Nicolas
; APPLICANT: IRM LLC
; TITLE OF INVENTION: Fluorogenic Enzyme Substrates and Uses
; FILE OF INVENTION: Thereof
; FILE REFERENCE: 021288-000410US
; CURRENT APPLICATION NUMBER: US/10/892,402
; CURRENT FILING DATE: 2004-07-14
; PRIOR APPLICATION NUMBER: US 60/487,464
; PRIOR FILING DATE: 2003-07-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 76
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: rhodamine protease substrate library peptide
US-10-892-402-76

Query Match      66.7%; Score 14; DB 6; Length 4;
Best Local Similarity 66.7%; Pred. No. 5.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 IPR 4
      :||
Db      1 LPR 3

RESULT 13
US-10-892-402-80
; Sequence 80, Application US/10892402
; GENERAL INFORMATION:
; APPLICANT: Harris, Jennifer L.
; APPLICANT: Damoiseaux, Robert
; APPLICANT: Backes, Bradley J.
; APPLICANT: Winsinger, Nicolas
; APPLICANT: IRM LLC
; TITLE OF INVENTION: Fluorogenic Enzyme Substrates and Uses
; FILE OF INVENTION: Thereof
; FILE REFERENCE: 021288-000410US
; CURRENT APPLICATION NUMBER: US/10/892,402
; CURRENT FILING DATE: 2004-07-14
; PRIOR APPLICATION NUMBER: US 60/487,464
; PRIOR FILING DATE: 2003-07-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 80
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
```

; OTHER INFORMATION: rhodamine protease substrate library peptide
US-10-892-402-80

Query Match 66.7%; Score 14; DB 6; Length 4;
Best Local Similarity 66.7%; Pred. No. 5.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IPR 4
: ||
Db 1 LPR 3

RESULT 14

US-10-892-402-84
; Sequence 84, Application US/10892402
; GENERAL INFORMATION:
; APPLICANT: Harris, Jennifer L.
; APPLICANT: Damoiseaux, Robert
; APPLICANT: Backes, Bradley J.
; APPLICANT: Winsinger, Nicolas
; APPLICANT: IRM LLC
; TITLE OF INVENTION: Fluorogenic Enzyme Substrates and Uses
; FILE OF INVENTION: Thereof
; FILE REFERENCE: 021288-000410US
; CURRENT APPLICATION NUMBER: US/10/892,402
; CURRENT FILING DATE: 2004-07-14
; PRIOR APPLICATION NUMBER: US 60/487,464
; PRIOR FILING DATE: 2003-07-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 84
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: rhodamine protease substrate library peptide
US-10-892-402-84

Query Match 66.7%; Score 14; DB 6; Length 4;
Best Local Similarity 66.7%; Pred. No. 5.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IPR 4
: ||
Db 1 LPR 3

RESULT 15

US-10-892-402-132
; Sequence 132, Application US/10892402
; GENERAL INFORMATION:
; APPLICANT: Harris, Jennifer L.
; APPLICANT: Damoiseaux, Robert
; APPLICANT: Backes, Bradley J.
; APPLICANT: Winsinger, Nicolas
; APPLICANT: IRM LLC
; TITLE OF INVENTION: Fluorogenic Enzyme Substrates and Uses
; FILE OF INVENTION: Thereof
; FILE REFERENCE: 021288-000410US
; CURRENT APPLICATION NUMBER: US/10/892,402
; CURRENT FILING DATE: 2004-07-14
; PRIOR APPLICATION NUMBER: US 60/487,464
; PRIOR FILING DATE: 2003-07-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 132
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: rhodamine protease substrate library peptide
US-10-892-402-132

Query Match 66.7%; Score 14; DB 6; Length 4;
Best Local Similarity 75.0%; Pred. No. 5.4e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPR 4
: ||
Db 1 RPR 4

Search completed: June 20, 2005, 16:48:01
Job time : 38 secs

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OM protein - protein search, using sw model

Run on: June 20, 2005, 16:01:11 ; Search time 23 Seconds
(without alignments)
16.733 Million cell updates/sec

Title: US-09-885-914B-3

Perfect score: 19

Sequence: 1 RVKR 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 86

Minimum DB seq length: 0
Maximum DB seq length: 4

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : PIR 79:.*
1: Pirl:.*
2: Pirl:.*
3: Pirl:.*
4: Pirl:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11	57.9	4	2 I40870	phospholipase C (E
2	8	42.1	4	2 I40804	endoglucanase F -
3	6	31.6	3	3 PQ0010	angiotensin-conver
4	6	31.6	3	3 S13894	histidinol dehydro
5	6	31.6	4	2 T46827	hypothetical prote
6	6	31.6	4	2 PT0721	T-cell receptor be
7	5	26.3	3	3 A22565	R-phycoerythrin al
8	5	26.3	3	3 E37196	bradykinin-potenti
9	5	26.3	3	3 F37196	growth-modulating
10	5	26.3	3	3 GKHU	bursin - chicken
11	5	26.3	3	3 A60898	antho-RFamide neur
12	5	26.3	4	1 ECXAA	phagocytosis-stimu
13	5	26.3	4	2 A02147	hypothetical prote
14	5	26.3	4	2 D41654	hypothetical prote
15	5	26.3	4	2 I40505	hypothetical prote
16	5	26.3	4	2 A25844	antho-RF amide neu
17	5	26.3	4	2 S39390	myosin-light-chain
18	5	26.3	4	2 I61883	protamine P1 - ora
19	5	26.3	4	2 E44823	synaptosomal-assoc
20	5	26.3	4	2 S47552	ubiquitin - rat
21	5	26.3	4	2 I37013	protamine P1 - Cer
22	5	26.3	4	2 I84439	protamine P1 - sav
23	5	26.3	4	2 FL0146	carbon-monoxide de
24	5	26.3	4	2 JQ1273	neuropeptide Antho
25	5	26.3	4	2 A35779	neuropeptide Antho
26	5	26.3	4	2 A60418	FWRFamide - polych
27	5	26.3	4	2 PT0534	T-cell receptor be
28	5	26.3	4	2 ECNK	cardioexcitatory n
29	4	21.1	4	2 A37832	phenol 2-monooxyge

ALIGNMENTS

RESULT 1

I40870

phospholipase C (EC 3.1.4.3) - Clostridium perfringens (fragment)

C;Species: Clostridium perfringens

C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 21-Jul-2000

C;Accession: I40870

R;Toyonaga, T.; Matsushita, O.; Katayama, S.; Minami, J.; Okabe, A.

Microbiol. Immunol. 36, 603-613, 1992

A;Title: Role of the upstream region containing an intrinsic DNA curvature in the negativ

A;Reference number: I40870; MUID:92396045; PMID:1522810

A;Accession: I40870

22K superhelical D
cell surface adhes
glucan 1,4-alpha-g
hypothetical prote
schwannomin - mous
branched-chain-ami
globulin IV alpha
ribosomal protein
D-mannosate hydrol
Ig heavy chain CRD
T-cell receptor be
T-cell receptor be
T-cell receptor be
gamma subunit of P
COI intron 16 prot
thyloliberin - she
thyloliberin - Bom
TRH-like tripeptid
gene p20K protein
T-cell receptor be
tyrosine protein k
cytochrome-c oxida
thyloliberin - pig
spinal cord peptid
spinal cord peptid
thyrotropin-releas
thyroglobulin - do
protein D - Escher
hypothetical prote
metallothionein-A
Ig heavy chain CRD
T-cell receptor be
protein-glutamine
pallidipin - assas
carbon-monoxide de
T-cell receptor be
T-cell receptor be
tyrosine-melanocyt
T-cell receptor be
T-cell receptor be
T-cell receptor be
starvation-induced
RPH-related neuro
Ig mu chain V regi
T-cell receptor be
biotin A - Citroba
achatin-I - giant
T-cell receptor be
T-cell receptor be
T-cell receptor be
T-cell receptor be
T-cell receptor be
T-cell receptor be
T-cell receptor be

30 4 21.1 4 2 A61300
31 4 21.1 4 2 B43848
32 4 21.1 4 2 A27897
33 4 21.1 4 2 T30569
34 4 21.1 4 2 I54357
35 4 21.1 4 2 A40135
36 4 21.1 4 2 S09478
37 4 21.1 4 2 S17255
38 3 15.8 4 2 I57745
39 3 15.8 4 2 PT0271
40 3 15.8 4 2 PT0633
41 3 15.8 4 2 PT0551
42 3 15.8 4 2 PT0697
43 2 10.5 4 2 A48360
44 2 10.5 4 2 I38888
45 1 5.3 3 3 RSHST
46 1 5.3 3 3 A92971
47 1 5.3 3 3 RHTDIO
48 1 5.3 3 3 A43391
49 1 5.3 3 3 I54112
50 1 5.3 3 3 PT0578
51 1 5.3 3 3 I78890
52 1 5.3 3 3 T13892
53 1 5.3 3 3 RHPGT
54 1 5.3 3 3 A23751
55 1 5.3 3 3 B23751
56 1 5.3 3 3 A33802
57 1 5.3 4 2 S18401
58 1 5.3 4 2 A41890
59 1 5.3 4 2 S43014
60 1 5.3 4 2 I51049
61 1 5.3 4 2 PT0240
62 1 5.3 4 2 A53284
63 1 5.3 4 2 A26209
64 1 5.3 4 2 S55238
65 1 5.3 4 2 PL0140
66 1 5.3 4 2 PT0645
67 1 5.3 4 2 PT0677
68 1 5.3 4 2 A32039
69 0 0.0 3 3 PT0636
70 0 0.0 3 3 PT0571
71 0 0.0 3 3 PT0622
72 0 0.0 3 3 S68328
73 0 0.0 4 2 S53508
74 0 0.0 4 2 A34626
75 0 0.0 4 2 A43959
76 0 0.0 4 2 B53284
77 0 0.0 4 2 I40697
78 0 0.0 4 2 A32480
79 0 0.0 4 2 PT0696
80 0 0.0 4 2 PT0711
81 0 0.0 4 2 PT0661
82 0 0.0 4 2 PT0712
83 0 0.0 4 2 PT0698
84 0 0.0 4 2 PT0706
85 0 0.0 4 2 PT0675
86 0 0.0 4 2 PT0566

A;Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A;Residues: 1-4 <RES>
A;Cross-references: EMBL:X62825; NID:g40622; PIDN:CAA44636.1; PID:g4377417
C;Genetics:
A;Gene: plc
C;Keywords: phosphoric diester hydrolase

Query Match 57.9%; Score 11; DB 2; Length 4;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VKR 4
:||
Db 1 MKR 3

RESULT 2
I40804
endoglucanase F - Clostridium thermocellum (fragment)
C;Species: Clostridium thermocellum
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C;Accession: I40804
R;Mishra, S.; Beguin, P.; Aubert, J.
J. Bacteriol. 173, 80-85, 1991

A;Title: Transcription of clostridium thermocellum endoglucanase genes celf and celd.
A;Reference number: I40804; MUID:91100322; PMID:1987137
A;Accession: I40804
A;Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A;Residues: 1-4 <RES>
A;Cross-references: UNIPROT:P26224; GB:M64363; NID:g144771
C;Genetics:
A;Gene: celf
A;Start codon: TTG

Query Match 42.1%; Score 8; DB 2; Length 4;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 VKR 4
:||
Db 1 MKK 3

RESULT 3
PQ0010
angiotensin-converting enzyme inhibitor (FLP-3) - common fig
N;Alternate names: ficus latex peptide 3
C;Species: Ficus carica (common fig)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: PQ0010
R;Maruyama, S.; Miyoshi, S.; Tanaka, H.
Agric. Biol. Chem. 53, 2763-2767, 1989
A;Title: Angiotensin I-converting enzyme inhibitors derived from Ficus carica.
A;Reference number: PQ0008
A;Accession: PQ0010
A:Molecule type: protein
A;Residues: 1-3 <MAR>
A;Experimental source: latex
C;Keywords: angiotensin-converting enzyme inhibitor

Query Match 31.6%; Score 6; DB 3; Length 3;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VK 3
:||
Db 2 VR 3

RESULT 4
S13894

histidinol dehydrogenase (EC 1.1.1.23) - wild cabbage (fragment)
C;Species: Brassica oleracea (wild cabbage)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: S13894
R;Nagai, A.; Scheidegger, A.
Arch. Biochem. Biophys. 284, 127-132, 1991
A;Title: Purification and characterization of histidinol dehydrogenase from cabbage.
A;Reference number: S13894; MUID:91112783; PMID:1989490
A;Accession: S13894
A:Molecule type: protein
A;Residues: 1-3 <NAG>
A;Experimental source: var. capitata
C;Keywords: dimer; NAD; oxidoreductase

Query Match 31.6%; Score 6; DB 3; Length 3;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VK 3
:||
Db 2 MK 3

RESULT 5
T46627
hypothetical protein c4 - loblolly pine
C;Species: Pinus taeda (loblolly pine)
C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 18-Feb-2000
C;Accession: T46627
R;Chang, S.; Puryea, J.; Funkhouser, E.A.; Newton, R.J.; Cairney, J.
submitted to the EMBL Data Library, July 1995
A;Description: Cloning of a chitinase homolog which lacks chitin binding sites and is do
A;Reference number: Z23105
A;Accession: T46627
A;Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A;Residues: 1-4 <CHA>
A;Cross-references: EMBL:U31309; NID:g974285; PID:g974292
A;Experimental source: strain s6PT2xs6PT3; 8 month seedlings

Query Match 31.6%; Score 6; DB 2; Length 4;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VK 3
:||
Db 1 MK 2

RESULT 6
PT0721
T-cell receptor beta chain V-D-J region (140-2K) - mouse (fragment)
C;Species: Mus musculus (mouse mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
C;Accession: PT0721
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0721
A;Status: translation not shown
A:Molecule type: DNA
A;Residues: 1-4 <FEE>
A;Cross-references: UNIPROT:Q8JZN5; UNIPROT:P54729; UNIPROT:Q8CBY1; UNIPROT:Q8COCO
A;Experimental source: newborn thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 31.6%; Score 6; DB 2; Length 4;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RV 2
|:

Db 2 RL 3

RESULT 7

A22565
R-phycoerythrin alpha-1 chain - red alga (Gastroclonium coulteri) (fragment)
C:Species: Gastroclonium coulteri
C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C:Accession: A22565
R:Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.
A:Reference number: A22565; MUID:85182601; PMID:3886644
A:Accession: A22565
A:Molecule type: protein
A:Residues: 1-3 <KLO>

Query Match 26.3%; Score 5; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 R 1
|
3 R 3

RESULT 8

E37196
bradykinin-potentiating peptide 5 - island jararaca
C:Species: Bothrops insularis (island jararaca)
C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 30-Jun-2001
C:Accession: E37196
R:Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.
J. Protein Chem. 9, 221-227, 1990
A:Title: Primary structure and biological activity of bradykinin potentiating peptides
A:Reference number: A37196; MUID:90351557; PMID:2386615
A:Accession: E37196
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-3 <CIN>
A:Keywords: pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 26.3%; Score 5; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 K 3
|
3 K 3

RESULT 9

F37196
bradykinin-potentiating peptide 6 - island jararaca
C:Species: Bothrops insularis (island jararaca)
C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C:Accession: F37196
R:Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.
J. Protein Chem. 9, 221-227, 1990
A:Title: Primary structure and biological activity of bradykinin potentiating peptides
A:Reference number: A37196; MUID:90351557; PMID:2386615
A:Accession: F37196
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-3 <CIN>
A:Keywords: pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 26.3%; Score 5; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 K 3
|
Db 2 K 2

RESULT 10

GKHU
growth-modulating peptide - human
C:Species: Homo sapiens (man)
C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Mar-2004
C:Accession: A01421
R:Schlesinger, D.H.; Pickart, L.; Thaler, M.M.
Experientia 33, 324-325, 1977
A:Title: Growth-modulating serum tripeptide is glycyl-histidyl-lysine.
A:Reference number: A01421; MUID:77162369; PMID:858356
A:Accession: A01421
A:Molecule type: protein
A:Residues: 1-3 <SCH>
A:Note: this serum tripeptide is found to stimulate growth of some cell types and to inhibit

Query Match 26.3%; Score 5; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 K 3
|
Db 3 K 3

RESULT 11

A60898
bursin - chicken
C:Species: Gallus gallus (chicken)
C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Mar-2004
C:Accession: A60898
R:Audhya, T.; Koon, D.; Heavner, G.; Viamontes, G.; Goldstein, G.
Science 231, 997-999, 1986
A:Title: Tripeptide structure of bursin, a selective B-cell-differentiating hormone of the
A:Reference number: A60898; MUID:86122916; PMID:3484838
A:Accession: A60898
A:Molecule type: protein
A:Residues: 1-3 <AUD>
A:Keywords: amidated carboxyl end; hormone
F:3/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 26.3%; Score 5; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 K 3
|
Db 1 K 1

RESULT 12

ECXAA
antho-RFamide neuropeptide - sea anemone (Anthopleura elegantissima)
C:Species: Anthopleura elegantissima
C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C:Accession: A26666
R:Grimmelikhuijzen, C.J.P.; Graff, D.
Proc. Natl. Acad. Sci. U.S.A. 83, 9817-9821, 1986
A:Title: Isolation of <Glu-Gly-Arg-Phe-NH2 (Antho-RFamide), a neuropeptide from sea anemone
A:Reference number: A26666; MUID:87092339; PMID:2879288
A:Accession: A26666
A:Molecule type: protein
A:Residues: 1-4 <GRI>
A:Cross-references: UNIPROT:P10419
A:Comment: The function of this peptide is not known but it could act as a transmitter at
C:Comment: Synthetic and natural peptides had identical properties.
C:Superfamily: RFamide neuropeptide
A:Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 26.3%; Score 5; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 K 3
|
Db 1 K 1

F:4/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 26.3%; Score 5; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 R 1
DB 3 R 3

RESULT 13

A02147
phagocytosis-stimulating peptide (tuftsin) - human
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C:Accession: A02147
R:Nishioaka, K.; Constantopoulos, A.; Satoh, P.S.; Najjar, V.A.
Biochem. Biophys. Res. Commun. 47, 172-179, 1972
A:Title: The characteristics, isolation and synthesis of the phagocytosis stimulating peptide
A:Reference number: A02147; PMID:72187087; PMID:4112769
A:Accession: A02147
A:Molecule type: protein
A:Residues: 1-4 <NIS>
A:Cross-references: UNIPROT:P01858
A:Note: a peptide having the same structure, physical properties, and biological activity
R:Fidalgo, B.V.; Najjar, V.A.
Biochemistry 6, 3386-3392, 1967
A:Reference number: A37502; PMID:68091045; PMID:4169272
A:Contents: annotation; immunoglobulin class
C:Comment: An IGG (called leucokinin) binds reversibly to the cell membrane of neutrophils
n is essential for maximum stimulation of the phagocytic activity of neutrophils.
C:Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 26.3%; Score 5; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 K 3
DB 2 K 2

RESULT 14

D41654
hypothetical protein (sodC 5' region) - Haemophilus parainfluenzae (fragment)
C:Species: Haemophilus parainfluenzae
C:Date: 12-Jun-1992 #sequence_revision 12-Jun-1992 #text_change 24-Feb-1995
C:Accession: D41654
R:Kroll, J.S.; Langford, P.R.; Loynds, B.M.
J. Bacteriol. 173, 7449-7457, 1991
A:Title: Copper-zinc superoxide dismutase of Haemophilus influenzae and Haemophilus parainfluenzae
A:Reference number: A41654; PMID:92041655; PMID:1938942
A:Accession: D41654
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-4 <KRO>

Query Match 26.3%; Score 5; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 R 1
DB 2 R 2

RESULT 15

I40505
hypothetical protein 3 (4 aa) - Bacillus stearothermophilus
C:Species: Bacillus stearothermophilus
C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 15-Oct-1999
C:Accession: I40505

R:Waye, M.M.; Winter, G.
Eur. J. Biochem. 158, 505-510, 1986
A:Title: A transcription terminator in the 5' non-coding region of the tyrosyl tRNA synthetase
A:Reference number: I40503; PMID:86274732; PMID:3525162
A:Accession: I40505
A:Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: DNA
A:Residues: 1-4 <RES>
A:Cross-references: EMBL:X04193; NID:G40233; PIDN:CAA27783.1; PID:G580944

Query Match 26.3%; Score 5; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 K 3
DB 4 K 4

Search completed: June 20, 2005, 16:34:36
Job time : 24 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2005, 15:59:16 ; Search time 109.5 Seconds
(without alignments)
18.706 Million cell updates/sec

Title: US-09-885-914B-3
Perfect score: 19
Sequence: 1 RVKR 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 26

Minimum DB seq length: 0
Maximum DB seq length: 4

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Uniprot 03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8	42.1	3	1 LUXE VIBFI	P24272 vibrio fisc
2	8	42.1	4	1 FYRI ANTEL	P58706 anthopleura
3	6	31.6	4	2 Q08433	Q08433 rattus sp.
4	5	26.3	3	1 GRWM HUMAN	P01157 homo sapien
5	5	26.3	4	1 DCMS PSECH	P19918 pseudomonas
6	5	26.3	4	1 PAR3 HIRME	P42562 hirudo medi
7	5	26.3	4	1 FAR4 HIRME	P42563 hirudo medi
8	5	26.3	4	1 FLRF HIRME	P58705 anthopleura
9	5	26.3	4	1 FLRN ANTEL	P42561 hirudo medi
10	5	26.3	4	1 FMRF MACNI	P58707 anthopleura
11	5	26.3	4	1 TUFT HUMAN	P01162 macrocallis
12	5	26.3	4	1 Q96ATO	P01858 homo sapien
13	5	26.3	4	2 Q96ATO	Q96ATO homo sapien
14	4	21.1	4	1 EOSI HUMAN	P02731 homo sapien
15	4	21.1	4	1 YLMI YEAST	P36515 saccharomyc
16	3	15.8	4	1 ILME SEPOF	P83568 sephia offic
17	1	5.3	3	1 THYL BOMOR	P62970 bombyx ori
18	1	5.3	3	1 THYL NOTVI	P62971 notophthalm
19	1	5.3	3	1 THYL PIG	P62968 sus scrofa
20	1	5.3	3	1 THYL SHEEP	P62969 ovis aries
21	1	5.3	4	1 DCML PSECH	P19916 pseudomonas
22	0	0.0	2	1 GWA SEPOF	P83570 sephia offic
23	0	0.0	4	1 ACHI ACHFU	P35904 achatina fu
24	0	0.0	4	1 OCPI OCTMI	P58648 octopus min
25	0	0.0	4	1 OCP3 OCTMI	P58649 octopus min
26	0	0.0	4	2 Q16047	Q16047 homo sapien

ALIGNMENTS

```
RESULT 1
LUXE_VIBFI STANDARD; PRT; 3 AA.
AC P24272;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Long-chain-fatty-acid-luciferin-component ligase (EC 6.2.1.19) (Acyl-
DE protein synthetase) (Fragment).
GN Name=luxe;
OS Vibrio fischeri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=668;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91072226; PubMed=2254256;
RA Swartzman E., Kapoor S., Graham A.P., Meighen E.A.;
RT "A new Vibrio fischeri lux gene precedes a bidirectional termination
RT site for the lux operon.";
RL J. Bacteriol. 172:6797-6802(1990).
CC -!- FUNCTION: Acyl-protein synthetase activates tetradecanoic acid. It
CC is a component of the fatty acid reductase complex responsible for
CC converting tetradecanoic acid to the aldehyde which serves as
CC substrate in the luciferase-catalyzed reaction.
CC -!- CATALYTIC ACTIVITY: ATP + an acid + protein = AMP + diphosphate +
CC an acyl-protein thioester.
CC -!- PATHWAY: Bioluminescent fatty acid reduction system; second step.
CC -!- SIMILARITY: Belongs to the luxE family.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
CC EMBL; MG2812; -; NOT ANNOTATED_CDS.
CC Ligase; Luminescence.
FT NON_TER 1
SQ SEQUENCE 3 AA; 374 MW; 6AA3303000000000 CRC64;

Query Match 42.1%; Score 8; DB 1; Length 3;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VK 3
Db :|
1 IK 2

RESULT 2
FYRI_ANTEL STANDARD; PRT; 4 AA.
AC P58706;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Anthopleura elegantissima (Sea anemone).
OS Anthopleura elegantissima (Sea anemone).
OC Eukaryota; Metazoa; Chnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nynanthaeae; Actiniidae; Anthopleura.
OX NCBI_TaxID=6110;
RN [1]
RP SEQUENCE.
RX MEDLINE=92270459; PubMed=1821096; DOI=10.1016/0196-9781(91)90190-Z;
RA Nothacker H.-P., Rinehart K.L. Jr., McFarlane I.D.,
RA Grimmelikhuijzen C.J.P.;
RT "Isolation of two novel neuropeptides from sea anemones: the unusual,
RT biologically active L-3-phenyllactyl-Tyr-Arg-Ile-NH2 and its des-
RT phenyllactyl fragment Tyr-Arg-Ile-NH2.";
RL Peptides 12:1165-1173 (1991).
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RN FUNCTION.
RX MEDLINE=93391436; PubMed=8397415;
RA McFarlane I.D., Hudman D., Nothacker H.-P., Gimmelikhuijzen C.J.P.;
RT "The expansion behaviour of sea anemones may be coordinated by two
RT inhibitory neuropeptides, Antho-Kamide and Antho-Riamide.";
RL Proc. R. Soc. Lond., B, Biol. Sci. 253:183-188(1993).
CC -!- FUNCTION: Inhibits spontaneous contractions in several muscle
CC groups. May be involved in the expansion phase of feeding
CC behaviour in sea anemones.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Neuron specific.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT CHAIN 1 4 Antho-Riamide I.
FT CHAIN 2 4 Antho-Riamide II.
FT MOD_RES 1 1 3-phenyllactic acid.
FT MOD_RES 4 4 Isoleucine amide.
SQ SEQUENCE 4 AA; 598 MW; 60441B59A0000000 CRC64;

Query Match 42.1%; Score 8; DB 1; Length 4;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RV 2
Db 3 RI 4

RESULT 3
Q08433
ID Q08433 PRELIMINARY; PRT; 4 AA.
AC Q08433
DT 01-NOV-1996 (TREMELrel. 01, Created)
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Bilirubin UDP-glucuronosyltransferase (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Gunn.
RX MEDLINE=91282758; PubMed=1840486;
RA Sato H., Aono S., Kashiwamata S., Koiwai O.;
RT "Genetic defect of bilirubin UDP-glucuronosyltransferase in the
RL hyperbilirubinemic Gunn rat.";
RL Biochem. Biophys. Res. Commun. 177:1161-1164(1991).
DR EMBL; S38636; AAB19259.1; -.
DR GO; GO:0016740; F:transferase activity; IEA.
KW Transferase.
FT NON_TER 4 4
SQ SEQUENCE 4 AA; 473 MW; 633732C420000000 CRC64;

Query Match 31.6%; Score 6; DB 2; Length 4;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VK 3
Db 3 LK 4

RESULT 4
GRWM_HUMAN
ID GRWM_HUMAN STANDARD; PRT; 3 AA.
AC P01157;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Growth-modulating peptide.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=77162369; PubMed=858356;
RA Schlesinger D.H., Pickart L., Thaler M.M.;
RT "Growth-modulating serum tripeptide is glycyl-histidyl-lysine.";
RL Experimentia 33:324-325(1977).
CC -!- MISCELLANEOUS: This serum tripeptide has been found to stimulate
CC growth of some cell types and to inhibit other types in vitro.
CC GO; GO:0001558; P:regulation of cell growth; NAS.
DR Direct protein sequencing.
KW SEQUENCE 3 AA; 340 MW; 6331E81000000000 CRC64;

Query Match 26.3%; Score 5; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 K 3
Db 3 K 3

RESULT 5
DCMS_PSECH
ID DCMS_PSECH STANDARD; PRT; 4 AA.
AC P19918;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Carbon monoxide dehydrogenase small chain (EC 1.2.99.2) (CO
DE dehydrogenase subunit S) (CO-DH S) (Fragment).
GN Name=cutS;
OS Pseudomonas carboxydohydrogena.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae.
OX NCBI_TaxID=290;
RN [1]
RP SEQUENCE.
RX MEDLINE=90055678; PubMed=2818128;
RA Kraut M., Hugendieck I., Herwig S., Meyer O.;
RT "Homology and distribution of CO dehydrogenase structural genes in
RT carboxydophilic bacteria.";
RL Arch. Microbiol. 152:335-341(1989).
CC -!- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon
CC dioxide.
CC -!- CATALYTIC ACTIVITY: CO + H(2)O + A = CO(2) + AH(2).
CC -!- COFACTOR: Binds 2 2Fe-2S clusters (By similarity).
CC -!- SUBUNIT: Heterotrimer consisting of a large, a medium and a small
CC subunit.
DR PIR; PLO146; PLO146.
KW 2Fe-2S; Direct protein sequencing; Iron; Iron-sulfur; Metal-binding;
KW Oxidoreductase.
FT NON_TER 4 4
SQ SEQUENCE 4 AA; 420 MW; 6DD33DD6F0000000 CRC64;

Query Match 26.3%; Score 5; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 K 3
Db 3 K 3

RESULT 6
FAR3_HIRME
ID FAR3_HIRME STANDARD; PRT; 4 AA.
AC P42562;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE FMRFamide-like neuropeptide YLRP-amide.

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OS Hirudo medicinalis (Medicinal leech).
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
 OC Arhynchobdellida; Hirudiniiformes; Hirudinidae; Hirudo.
 OX NCBI_TaxID=6421;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92195954; PubMed=1686933; DOI=10.1016/0196-9781(91)90035-N;
 RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
 RT "Identification of RFamide neuropeptides in the medicinal leech.";
 RL Peptides 12:897-908(1991).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide) family.
 CC Amidation; Direct protein sequencing; Neuropeptide.
 KW MOD_RES 4 4 Phenylalanine amide.
 SQ SEQUENCE 4 AA; 598 MW; 69D4073B30000000 CRC64;
 Query Match 26.3%; Score 5; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06; Mismatches 0; Indels 0; Gaps 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 R 1
 Db 3 R 3
 RESULT 7
 ID_FARP_HIRME STANDARD; PRT; 4 AA.
 AC P42563;
 DT 01-NOV-1995. (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE FMRFamide-like neuropeptide YMRP-amide.
 OS Hirudo medicinalis (Medicinal leech).
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
 OC Arhynchobdellida; Hirudiniiformes; Hirudinidae; Hirudo.
 OX NCBI_TaxID=6421;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92195954; PubMed=1686933; DOI=10.1016/0196-9781(91)90035-N;
 RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
 RT "Identification of RFamide neuropeptides in the medicinal leech.";
 RL Peptides 12:897-908(1991).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide) family.
 CC Amidation; Direct protein sequencing; Neuropeptide.
 KW MOD_RES 4 4 Phenylalanine amide.
 SQ SEQUENCE 4 AA; 616 MW; 69D4068B30000000 CRC64;
 Query Match 26.3%; Score 5; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06; Mismatches 0; Indels 0; Gaps 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 R 1
 Db 3 R 3
 RESULT 8
 ID_FFKA_ATEL STANDARD; PRT; 4 AA.
 AC P58705;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Antho-KAamide.
 OS Anthopleura elegantissima (Sea anemone).
 OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
 OC Nynanthaeae; Actinidae; Anthopleura.
 OX NCBI_TaxID=6110;
 RN [1]

RP SEQUENCE.
 RX MEDLINE=92028852; PubMed=1681803;
 RA Nothacker H.-P., Rinehart K.L. Jr., Grimmelikhuijzen C.J.P.;
 RT "Isolation of L-3-phenyllactyl-Phe-Lys-Ala-NH2 (Antho-KAamide), a novel neuropeptide from sea anemones.";
 RL Biochem. Biophys. Res. Commun. 179:1205-1211(1991).
 RN [2]
 RP FUNCTION.
 RX MEDLINE=93391436; PubMed=8397415;
 RA McFarlane I.D., Hudman D., Nothacker H.-P., Grimmelikhuijzen C.J.P.;
 RT "The expansion behaviour of sea anemones may be coordinated by two inhibitory neuropeptides, Antho-KAamide and Antho-RKamide.";
 RL Proc. R. Soc. Lond., B, Biol. Sci. 253:183-188(1993).
 CC -1- FUNCTION: Inhibits spontaneous contractions in several muscle groups. May be involved in the expansion phase of feeding behaviour in sea anemones.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Neuron specific.
 DR PIR; JQ1273; JQ1273.
 KW Amidation; Direct protein sequencing; Neuropeptide.
 FT MOD_RES 1 1 3-phenyllactic acid.
 FT MOD_RES 4 4 Alanine amide.
 SQ SEQUENCE 4 AA; 512 MW; 6DD339C9A0000000 CRC64;
 Query Match 26.3%; Score 5; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06; Mismatches 0; Indels 0; Gaps 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 K 3
 Db 3 K 3
 RESULT 9
 ID_FLRF_HIRME STANDARD; PRT; 4 AA.
 AC P42561;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE FLRFamide.
 OS Hirudo medicinalis (Medicinal leech), and
 OS Helisoma trivolvis (Snail).
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
 OC Arhynchobdellida; Hirudiniiformes; Hirudinidae; Hirudo.
 OX NCBI_TaxID=6421, 27815;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=H.medicalinalis;
 RX MEDLINE=92195954; PubMed=1686933; DOI=10.1016/0196-9781(91)90035-N;
 RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
 RT "Identification of RFamide neuropeptides in the medicinal leech.";
 RL Peptides 12:897-908(1991).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=H.trivolvis; TISSUE=Kidney;
 RX MEDLINE=94286417; PubMed=7912428; DOI=10.1016/0196-9781(94)90166-X;
 RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
 RT "FMRFamide-related peptides from the kidney of the snail, Helisoma trivolvis.";
 RL Peptides 15:31-36(1994).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide) family.
 KW Amidation; Direct protein sequencing; Neuropeptide.
 FT MOD_RES 4 4 Phenylalanine amide.
 SQ SEQUENCE 4 AA; 582 MW; 69D40729A000000000 CRC64;
 Query Match 26.3%; Score 5; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06; Mismatches 0; Indels 0; Gaps 0;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 R 1

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Db          3 R 3

RESULT 10
FLRN ANTEL          STANDARD;          PRT;          4 AA.
AC P58707;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Antho-RNamide.
OS Anthopleura elegantissima (Sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nynantheae; Actiniidae; Anthopleura.
OX NCBI_TaxID=6110;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RX MEDLINE=90319122; PubMed=1973541;
RA Grimmelikhuijzen C.J.P., Rinehart K.L. Jr., Jacob E., Graff D.,
RA Reinecheid R.K., Nothacker H.-P., Staley A.L.;
RT "Isolation of L-3-phenylalanyl-Leu-Arg-Asn-NH2 (Antho-RNamide), a sea
RT anemone neuropeptide containing an unusual amino-terminal blocking
RT group."
RL Proc. Natl. Acad. Sci. U.S.A. 87:5410-5414 (1990).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Neuron specific.
CC -1- MASS SPECTROMETRY: MW=549.3; METHOD=FAB; RANGE=1-4; NOTE=Ref.1.
DR PIR; A35779; A35779.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD_RES 1 1 3-phenylalactic acid.
FT MOD_RES 4 4 Asparagine amide.
SQ SEQUENCE 4 AA; 549 MW; 64540729A0000000 CRC64;

Query Match 26.3%; Score 5; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 R 1
Db 3 R 3

RESULT 11
PMRF_MACNI
ID PMRF_MACNI          STANDARD;          PRT;          4 AA.
AC P01162;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE PMRFamide (Peak C) (Cardioexcitatory neuropeptide).
OS Macrocaltista nimboza (Sun-ray clam),
OS Nereis virens (Sandworm),
OS Hirudo medicinalis (Medicinal leech), and
OS Helisoma trivolvis (Snail).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroidea;
OC Veneroidea; Veneridae; Macrocallista.
OX NCBI_TaxID=6594, 6353, 6421, 27815;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC SPECIES=M.nimboza; TISSUE=Cerebral pedal, and Visceral ganglion;
RX MEDLINE=77215956; PubMed=877582;
RA Price D.A., Greenberg M.J.;
RT "Structure of a molluscan cardioexcitatory neuropeptide."
RL Science 197:670-671 (1977).
RN [2]
RP SEQUENCE, AND CHARACTERIZATION.
RC SPECIES=M.nimboza; TISSUE=Ganglion;
RX MEDLINE=78012038; PubMed=909875;
RA Price D.A., Greenberg M.J.;
RT "Purification and characterization of a cardioexcitatory neuropeptide
RT from the central ganglia of a bivalve mollusc."
RL Prep. Biochem. 7:261-281 (1977).

RN [3]
RP SEQUENCE.
RC SPECIES=N.virens;
RX MEDLINE=90259866; PubMed=2342992; DOI=10.1016/0196-9781(90)90113-J;
RA Krajniak K.G., Price D.A.;
RT "Authentic K-FRamide is present in the polychaete Nereis virens."
RL Peptides 11:75-77 (1990).
RN [4]
RP SEQUENCE.
RC SPECIES=H.medicinalis;
RX MEDLINE=92195954; PubMed=1686933; DOI=10.1016/0196-9781(91)90035-N;
RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT "Identification of RFamide neuropeptides in the medicinal leech."
RL Peptides 12:897-908 (1991).
RN [5]
RP SEQUENCE.
RC SPECIES=H.trivolvis; TISSUE=Kidney;
RX MEDLINE=94286417; PubMed=7912428; DOI=10.1016/0196-9781(94)90166-X;
RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
RT "FMRFamide-related peptides from the kidney of the snail, Helisoma
RT trivolvis."
RL Peptides 15:31-36 (1994).
CC -1- FUNCTION: Myoactive; cardioexcitatory substance. Pharmacological
CC activities include augmentation, induction, and regularization of
CC cardiac contraction.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC family.
DR PIR; A01426; ECNK.
DR PIR; A60418; A60418.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD_RES 4 4 Phenylalanine amide.
SQ SEQUENCE 4 AA; 600 MW; 69D40699A0000000 CRC64;

Query Match 26.3%; Score 5; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 R 1
Db 3 R 3

RESULT 12
TUFT_HUMAN
ID TUFT_HUMAN          STANDARD;          PRT;          4 AA.
AC P01858;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Phagocytosis-stimulating peptide (Tuftsin).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE
RX MEDLINE=72187087; PubMed=4112769;
RA Nishioka K., Constantopoulos A., Satoh P.S., Najjar V.A.;
RT "The characteristics, isolation and synthesis of the phagocytosis
RT stimulating peptide tuftsin."
RL Biochem. Biophys. Res. Commun. 47:172-179 (1972).
RN [2]
RP IMMUNOGLOBULIN CLASS.
RX MEDLINE=68091045; PubMed=4169272;
RA Fidalgo B.V., Najjar V.A.;
RT "The physiological role of the lymphoid system. VI. The stimulatory
RT effect of leucophilic gamma globulin (leucokinin) on the phagocytic
RT activity of human polymorphonuclear leucocyte."
RL Biochemistry 6:3386-3392 (1967).
CC -1- MISCELLANEOUS: An IGG (called leucokinin) binds reversibly to the
CC cell membrane of neutrophils in the blood. Leucokininase on the
CC membrane releases the active peptide tuftsin from the gamma chain.

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CC Tuftsin is essential for maximum stimulation of the phagocytic
 CC activity of neutrophils.
 DR PIR; A02147; A02147.
 DR MIM; 191150; -.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006909; P:phagocytosis; NAS.
 DR KW Direct protein sequencing.
 SQ SEQUENCE 4 AA; 501 MW; 74176321C0000000 CRC64;
 Query Match 26.3%; Score 5; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 K 3
 Db 2 K 2
 RESULT 13
 Q96A70 PRELIMINARY; PRT; 4 AA.
 ID Q96A70
 AC Q96A70;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE FLJ30656 protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins P.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T.J., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RL and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RA Strausberg R.;
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR ENBL; BC016791; AAH16791.2; -.
 SQ SEQUENCE 4 AA; 512 MW; 633DCB56F0000000 CRC64;
 Query Match 26.3%; Score 5; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 K 3
 Db 4 K 4
 RESULT 14
 E0S1_HUMAN

ID E0S1_HUMAN STANDARD; PRT; 4 AA.
 AC P02731;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Eosinophilic tetrapeptides.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE
 RX MEDLINE=76078412; PubMed=1060093;
 RA Goetzl E.J., Austen K.F.;
 RT "Purification and synthesis of eosinophilic tetrapeptides of
 RT human lung tissue: identification as eosinophil chemotactic factor of
 RT anaphylaxis";
 RL Proc. Natl. Acad. Sci. U.S.A. 72:4123-4127(1975).
 CC -I- MISCELLANEOUS: These peptides are released from mast cells in lung
 CC (and other tissues) during hypersensitivity reactions
 CC (anaphylaxis). Their activities, preferentially affecting
 CC eosinophils, include chemotaxis, chemotactic deactivation, release
 CC of enzymes, and stimulation of the hexose monophosphate shunt.
 CC GO: GO:0006935; P:chemotaxis; IDA.
 DR GO: GO:0006955; P:immune response; IDA.
 KW Direct protein sequencing.
 FT VARIANT 1
 FT 1 V -> A (in other peptide).
 SQ SEQUENCE 4 AA; 390 MW; 6B05B862A0000000 CRC64;
 Query Match 21.1%; Score 4; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 V 2
 Db 1 V 1
 RESULT 15
 YLMI YEAST
 ID YLMI YEAST STANDARD; PRT; 4 AA.
 AC P36515;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Mitochondrial 60S ribosomal protein L1 (Yml1) (Fragment).
 GN Name=Yml1;
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=91285106; PubMed=2060626; DOI=10.1016/0014-5793(91)80759-V;
 RA Grohmann L., Graack H.-R., Kruff V., Choi T., Goldschmidt-Reisin S.,
 RA Kitakawa M.;
 RT "Extended N-terminal sequencing of proteins of the large ribosomal
 RT subunit from yeast mitochondria";
 RL FEBS Lett. 284:51-56(1991).
 CC -I- FUNCTION: Putative component of the large subunit of mitochondrial
 CC ribosome.
 CC -I- SUBCELLULAR LOCATION: Mitochondrial.
 DR PIR; S17255; S17255.
 KW Direct protein sequencing; Mitochondrion; Ribosomal protein.
 FT NON_TER 4
 SQ SEQUENCE 4 AA; 402 MW; 7771B2D5D0000000 CRC64;
 Query Match 21.1%; Score 4; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 V 2

Db 2 V 2

Search completed: June 20, 2005, 16:33:43
Job time : 109.5 secs

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OM protein - protein search, using sw model

Run on: June 20, 2005, 14:16:51 ; Search time 113.5 Seconds
(without alignments)
13.630 Million cell updates/sec

Title: US-09-885-914B-3

Perfect score: 19

Sequence: 1 RVKR 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 19815

Minimum DB seq length: 0

Maximum DB seq length: 4

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : A Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	100.0	4	6	Aae35573 Furin cle
2	19	100.0	4	8	Adj57391 Furin inh
3	16	84.2	4	2	Aay30777 Peptide u
4	16	84.2	4	3	Aay84215 Amino aci
5	16	84.2	4	4	Aab97408 Site-1 pr
6	16	84.2	4	4	Aab97427 Site-1 pr
7	16	84.2	4	5	Aae24432 Transport
8	16	84.2	4	5	Aao14861 Furin sub
9	16	84.2	4	6	Abp71148 Human pro
10	16	84.2	4	6	Adai10587 Eglin c v
11	16	84.2	4	7	Adh84924 Tetrapept
12	16	84.2	4	8	Adg19004 Multimeri
13	16	84.2	4	8	Adj57390 Peptide f
14	15	78.9	4	2	Aar37629 Sequence
15	15	78.9	4	2	Aar60593 proins.RT
16	15	78.9	4	5	Aau75632 Human myo
17	15	78.9	4	5	Aau78849 Human ins
18	15	78.9	4	5	Aae18671 Zebra fis
19	15	78.9	4	5	Aao17049 Furin sit
20	15	78.9	4	6	Abg73570 Human pro
21	15	78.9	4	6	Aao30152 Spectrozy
22	15	78.9	4	6	Aae29827 Spectrozy
23	15	78.9	4	6	Aae29796 Spectrozy
24	15	78.9	4	6	Adai10588 Eglin c v
25	15	78.9	4	6	Adb17421 Human ins

26	15	78.9	4	7	ABU10024
27	15	78.9	4	7	ADB97569 Protease
28	15	78.9	4	8	ADI28884 Human ser
29	15	78.9	4	8	ADJ57392 Furin inh
30	14	73.7	4	1	AAP20059 Enzyme su
31	14	73.7	4	2	Aar37635 Sequence
32	14	73.7	4	2	Aar85940 Peptidase
33	14	73.7	4	3	Aay44372 Tetraresi
34	14	73.7	4	4	AAB67720 Amino aci
35	14	73.7	4	4	AAU07641 Wild-type
36	14	73.7	4	4	AAM52826 HIV gp120
37	14	73.7	4	5	AAM52826 HIV gp120
38	14	73.7	4	5	Aae18624 Heparin b
39	14	73.7	4	5	ABG31272 Human fac
40	14	73.7	4	5	AAE24598 Yeast Kex
41	14	73.7	4	6	ABP98103 Amino aci
42	14	73.7	4	6	ABR40173 Marburg v
43	14	73.7	4	7	ADH10700 Streptomy
44	14	73.7	4	8	ADQ80880 Subtilisi
45	13	68.4	4	2	AAR37630 Sequence
46	13	68.4	4	2	AAR48281 Nuclea r
47	13	68.4	4	2	AAR60559 Tissue pl
48	13	68.4	4	2	AAR60594 proins.RQ
49	13	68.4	4	2	AAR51491 Human A-m
50	13	68.4	4	2	AAR52965 Human A-m
51	13	68.4	4	2	AAR64811 ScFv-Lys
52	13	68.4	4	2	AAR65180 Dibasic a
53	13	68.4	4	2	AAW71193 Peptide u
54	13	68.4	4	2	AAW70904 Amino aci
55	13	68.4	4	2	AAW44279 Human thy
56	13	68.4	4	2	AAW96353 Nucleus 1
57	13	68.4	4	3	AAV57104 Linker am
58	13	68.4	4	3	AAV82083 HIV 168P
59	13	68.4	4	3	AAV82085 HIV enhan
60	13	68.4	4	3	AB14217 HIV SF162
61	13	68.4	4	4	AAE00920 Cleavage
62	13	68.4	4	4	AB72635 Mammalian
63	13	68.4	4	4	AB72639 Mammalian
64	13	68.4	4	4	AB62231 PA protei
65	13	68.4	4	5	AAE14288 Thymosin
66	13	68.4	4	5	AAU78847 Human ins
67	13	68.4	4	5	AB77181 Human mat
68	13	68.4	4	5	ABE24419 Transport
69	13	68.4	4	5	ABG31270 Human fac
70	13	68.4	4	5	ABO17055 Peptide a
71	13	68.4	4	5	ABO09213 HIV Env c
72	13	68.4	4	5	AAW52115 Anthrax P
73	13	68.4	4	5	ABG73639 PERV type
74	13	68.4	4	5	ABG92988 Nucleus 1
75	13	68.4	4	6	ABR57047 Furin-rec
76	13	68.4	4	6	ABP98107 Amino aci
77	13	68.4	4	6	ABU08964 ADAM meta
78	13	68.4	4	6	ABP56583 Endoplasm
79	13	68.4	4	6	ABP71147 Human pro
80	13	68.4	4	6	ADB17417 Human ins
81	13	68.4	4	7	ADB87742 HIV-1 str
82	13	68.4	4	7	ADC13968 Rheumatol
83	13	68.4	4	7	ADC73270 Yeast Int
84	13	68.4	4	7	ADD66262 HIV-1 Env
85	13	68.4	4	8	ADF61758 Exemplary
86	13	68.4	4	8	ADG18991 Multimeri
87	13	68.4	4	8	ADI05537 Novel ade
88	13	68.4	4	8	ADJ57388 Peptide f
89	13	68.4	4	8	ADJ58925 Human pro
90	13	68.4	4	8	ADK42329 Antibacte
91	13	68.4	4	8	ADP44031 Human thy
92	13	68.4	4	8	ADQ30899 Newcastle
93	13	68.4	4	8	ADS82099 Cleavage
94	12	63.2	4	2	AAR37631 Sequence
95	12	63.2	4	2	AAR38742 KEX2 clea
96	12	63.2	4	2	AAR59927 Alpha 1-a
97	12	63.2	4	2	AAR60595 proins.KT
98	12	63.2	4	2	AAR90378 Synthetic

99 12 63.2 4 2 AAW25085 Aaw25085 Protein C
100 12 63.2 4 2 AAY20463 Aay20463 Human mic

ALIGNMENTS

RESULT 1
AAE35573 standard; peptide; 4 AA.

XX AC AAE35573;
XX AC AAE35573;
XX DT 17-JUN-2003 (first entry)
XX DE Furin cleavable linker peptide.
XX KW Fusion agent; immunogenic; proliferative disease; infectious disease;
XX KW cancer; therapy; vaccine; melanoma; Trojan antigen; TA.
XX OS Unidentified.
XX PN WO200294994-A2.
XX PD 28-NOV-2002.
XX PF 20-MAY-2002; 2002WO-US015992.
XX PR 18-MAY-2001; 2001US-0291874P.
XX PA (MAYO-) MAYO FOUND MEDICAL EDUCATION RES.
XX PI Celis E;
XX DR WPI; 2003-140367/13.
XX PT Fusion agent useful for preventing and treating an infectious disease, or
XX PT a proliferative disease, such as cancer, comprises a transport domain,
XX PT two cleavage sites, a peptide epitope and a biologically active agent.
XX PS Example 1; Page 37; 72pp; English.

XX CC The invention relates to a fusion agent (Trojan antigen; TA) comprising a
XX CC transport domain, two cleavage sites, a peptide epitope recognised by an
XX CC antigen-specific receptor on an effector T-lymphocyte precursor cell and
XX CC a biologically active agent, where there is a cleavage site between the
XX CC peptide epitope and the biologically active agent and between each
XX CC biologically active agent. The fusion agent is used to make a cell
XX CC immunogenic or antigenic. It is also useful for preventing and treating
XX CC an infectious disease such as viral, bacterial, protozoal, fungal or
XX CC yeast disease, or proliferative disease such as cancer (e.g. melanoma,
XX CC neural tissue, gastrointestinal, breast, lung, ovarian, testicular,
XX CC prostate, cervical, bladder, liver, renal, bone, haematological
XX CC or vascular tissue cancer). The invention is used as vaccines. The
XX CC present sequence is furin cleavable linker peptide. This peptide is used
XX CC in the exemplification of the invention

XX SQ Sequence 4 AA;

Query Match 100.0%; Score 19; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVKR 4
DB 1 RVKR 4

RESULT 2
ADJ57391 standard; peptide; 4 AA.
XX AC ADJ57391;
XX AC ADJ57391;

XX 06-MAY-2004 (first entry)
XX Furin inhibitor peptide.
XX DE
XX KW Convertase; inhibitor; furin; antiinflammatory; vulnerary;
XX KW ophthalmological; dermatological; nephrotropic; hepatotropic; vasotropic;
XX KW antifertility; respiratory-gen.; cardiant; CNS-gen.; cerebroprotective;
XX KW neuroprotective; nootropic; cytostatic; antiarthritic;
XX KW antiarteriosclerotic.
XX OS Unidentified.
XX OS
XX FH Key Location/Qualifiers
XX FT Modified-site 1 /note= "dec-Arg"
XX FT Modified-site 4 /note= "Arg-cmk"
XX PN WO2004009113-A1.
XX PD 29-JAN-2004.
XX PF 23-JUL-2003; 2003WO-GB003159.
XX PR 24-JUL-2002; 2002GB-00017136.
XX PA (RENO-) RENOVO LTD.
XX PI Ferguson MWJ, Brunner G;
XX DR WPI; 2004-180270/17.
XX PT Use of a convertase inhibitor in the manufacture of a medicament for
XX PT reducing scarring during the healing of wounds or reducing fibrosis in
XX PT the treatment of fibrotic conditions.
XX PS Example; Page 28; 43pp; English.

XX CC The present sequence is that of a furin inhibitor peptide. This was used
XX CC in an example from the invention which showed that furin-like enzymes are
XX CC involved in platelet-mediated latent transforming growth factor-beta (TGF
XX CC -beta) activation. The inventors have established that convertase enzymes
XX CC such as furin act, both extracellularly and intracellularly, to cause the
XX CC activation of latent transforming growth factor-beta (TGF-beta) in the
XX CC extracellular space at the site of a wound of a fibrotic conditions.
XX CC Thus, the present invention relates to use of convertase inhibitors for
XX CC the reduction of scarring during the healing of wounds, for reducing to
XX CC fibrosis in the treatment of fibrotic conditions, for treating wounds to
XX CC prevent scar formation, for preventing scarring of the eye, nervous
XX CC tissue or intestines, dermal scarring and scarring following a burn. The
XX CC fibrotic condition is a fibrotic disorder such as glomerulonephritis,
XX CC cirrhosis of the liver, fibrotic disease, adhesions and restenosis (all
XX CC claimed). The convertase inhibitor can also be used for the treatment of
XX CC hypertrophic and keloid scars, scarring in the heart, scarring of the gut,
XX CC scarring in the pelvis in the region of the fallopian tubes leading to
XX CC infertility, scarring following injury to the muscles, scarring or
XX CC fibrosis following injury to tendons and ligaments, which can result in
XX CC serious loss of function, liver fibrosis, pulmonary fibrosis,
XX CC scleroderma, myocardial hibernation, fibrosis following myocardial
XX CC infarction, central nervous system fibrosis following a stroke or
XX CC neurodegenerative disorders (e.g. Alzheimer's disease), proliferative
XX CC vitreoretinopathy, arthritis, arteriosclerosis and cancer.

XX SQ Sequence 4 AA;

Query Match 100.0%; Score 19; DB 8; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVKR 4
DB 1 RVKR 4

RESULT 3
 AAY30777
 ID AAY30777 standard; peptide; 4 AA.
 XX
 AC AAY30777;
 XX
 DT 25-NOV-1999 (first entry)
 XX
 DE Peptide used to determine substrate specificity of an endo-type protease.
 XX
 KW Endo-type cysteine protease; cod fish milk; food; beverage.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1 /note= "protected with -BOC"
 FT Modified-site 4 /note= "-MAC attached"
 FT
 XX JP11225756-A.
 XX
 PD 24-AUG-1999.
 XX
 PF 10-FEB-1998; 98JP-00042973.
 XX
 PR 10-FEB-1998; 98JP-00042973.
 XX
 PA (HASE) HASEGAWA CO LTD.
 XX
 DR WPI; 1999-553905/47.
 XX
 PT New cysteine protease - useful in food/beverage products and pharmaceuticals.
 PT
 PS Disclosure; Page 4; 9pp; Japanese.
 XX
 CC The specification describes an endo-type cysteine protease that has substrate specificity and cleaves the C terminus side of the sequence of Lys-Arg and Arg-Arg. The enzyme has the molecular weight of 72,000 based on SDS-PAGE and an isoelectric point of 5.22. The endo-type cysteine protease is obtained from cod fish milk. The enzyme is used in food and beverage products and pharmaceuticals. The present sequence represents a peptide used to determine specificity of the enzyme
 XX
 SQ Sequence 4 AA;
 Query Match 84.2%; Score 16; DB 2; Length 4;
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RVKR 4
 ||:|
 Db 1 RVRK 4
 RESULT 4
 AAY84215
 ID AAY84215 standard; peptide; 4 AA.
 XX
 AC AAY84215;
 XX
 DT 03-JUL-2000 (first entry)
 XX
 DE Amino acid sequence of a peptide.
 XX
 KW Modulator; sterol-regulated Site-1 protease; cholesterol;
 KW sterol regulatory element binding protein; SREBP; lipid synthesis;
 KW fatty acid biosynthesis; site-1 protease; protease inhibitor;
 KW serum cholesterol; hypercholesterolemia; lipid metabolism.
 XX

OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1 /note= "Boc attached"
 FT Misc-difference 4 /note= "attached to MCA"
 FT
 XX WO200009677-A2.
 XX
 PD 24-FEB-2000.
 XX
 PF 13-AUG-1999; 99WO-US018544.
 XX
 PR 14-AUG-1998; 98US-0096571P.
 PR 23-JUL-1999; 99US-00360237.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 PA (BROW/) BROWN M S.
 PA (CHEN/) CHENG D.
 PA (ESPE/) ESPENSHADE P J.
 PA (GOLD/) GOLDSTEIN J L.
 PA (RAWS/) RAWSON R B.
 PA (SAKA/) SAKAI J.
 XX
 PI Brown MS, Cheng D, Espenshade PJ, Goldstein JL, Rawson RB;
 PI Sakai J;
 XX
 DR WPI; 2000-224327/19.
 XX
 PT Novel assay for identifying modulators of sterol-regulated Site-1 protease useful for the treatment of hypercholesterolemia, involves identifying an agent capable of down regulating Site-1 protease activity.
 PT
 XX Example 11; Page 106; 172pp; English.
 XX
 CC The specification describes a method for identifying modulators of a sterol-regulated Site-1 protease. Site-1 protease cleaves sterol regulatory element binding proteins (SREBPs) in the endoplasmic reticulum, initiating release from membranes and activating lipid synthesis. The modulators therefore also modulate cholesterol and fatty acid biosynthesis. The method comprises selecting an agent capable of down regulating Site-1 protease and formulating a composition comprising the agent. The site-1 protease inhibitors are useful for treating a patient for elevated serum cholesterol. Diseases treated include hypercholesterolemia and other lipid metabolism associated conditions. The present sequence was used in the course of the invention
 XX
 SQ Sequence 4 AA;
 Query Match 84.2%; Score 16; DB 3; Length 4;
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RVKR 4
 ||:|
 Db 1 RVRK 4
 RESULT 5
 AAB97408
 ID AAB97408 standard; peptide; 4 AA.
 XX
 AC AAB97408;
 XX
 DT 27-JUL-2001 (first entry)
 XX
 DE Site-1 protease inhibition method related peptide #2.
 XX
 KW Site-1 protease; S1P; sterol regulatory element binding protein; SREBP;
 KW fatty acid synthesis; cholesterol homeostasis; triglyceride.
 XX
 OS Synthetic.

XX Key Location/Qualifiers
 FT Modified-site 1 /label= OTHER
 FT Modified-site 4 /note= "modified by t-butyloxycarbonyl"
 FT Modified-site 4 /label= OTHER
 FT Modified-site 4 /note= "modified by 4-methyl-coumaryl-7-amide"
 XX WO200127138-A2.
 PN 19-APR-2001.
 PD 11-OCT-2000; 2000WO-US028428.
 PP 13-OCT-1999; 99US-0159236P.
 PR (TULA-) TULARIK INC.
 PA (UYTE-) UNIV TEXAS SOUTHWESTERN MEDICAL CENT DAL.
 XX Jaen JC, Li L, Brown MS, Goldstein JL, Cheng D;
 PI WPI; 2001-328425/34.
 DR Peptide derivatives, useful as S1 protease inhibitors for modulating
 XX expression of genes regulated by SREBP transcription factors and for
 PT treating conditions associated with abnormal cholesterol or lipid
 PT homeostasis.
 XX Example; Page 24; 41pp; English.
 PS The present invention describes a number of peptide derivatives which are
 CC capable of modulating Site-1 protease (S1P). S1P initiates the release of
 CC sterol regulatory element binding proteins (SREBPs), which control the
 CC synthesis of fatty acids and cholesterol. The peptide derivatives of the
 CC invention are, therefore, useful in the modulation of cholesterol
 CC homeostasis and in the treatment of conditions associated with abnormal
 CC levels of plasma cholesterol, lipoproteins or triglycerides. The present
 CC sequence is a peptide used in the exemplification of the invention
 XX Sequence 4 AA;
 SQ Query Match 84.2%; Score 16; DB 4; Length 4;
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RVKR 4
 DB 1 RVR 4
 RESULT 6
 AAB97427
 ID AAB97427 standard; peptide; 4 AA.
 AC AAB97427;
 XX 27-JUL-2001 (first entry)
 DT Site-1 protease fluorogenic peptide assay substrate #10.
 DE Site-1 protease; S1P; sterol regulatory element binding protein; SREBP;
 KW fatty acid synthesis; cholesterol homeostasis; triglyceride.
 XX Unidentified.
 OS Key Location/Qualifiers
 XX Modified-site 1 /label= OTHER
 FT Modified-site 4 /note= "modified by t-butyloxycarbonyl"
 FT Modified-site 4 /label= OTHER
 FT Modified-site 4 /note= "modified by 4-methyl-coumaryl-7-amide"

XX WO200127138-A2.
 PN 19-APR-2001.
 PD 11-OCT-2000; 2000WO-US028428.
 PP 13-OCT-1999; 99US-0159236P.
 PR (TULA-) TULARIK INC.
 PA (UYTE-) UNIV TEXAS SOUTHWESTERN MEDICAL CENT DAL.
 XX Jaen JC, Li L, Brown MS, Goldstein JL, Cheng D;
 PI WPI; 2001-328425/34.
 DR Peptide derivatives, useful as S1 protease inhibitors for modulating
 XX expression of genes regulated by SREBP transcription factors and for
 PT treating conditions associated with abnormal cholesterol or lipid
 PT homeostasis.
 XX Example; Page 27; 41pp; English.
 PS The present invention describes a number of peptide derivatives which are
 CC capable of modulating Site-1 protease (S1P). S1P initiates the release of
 CC sterol regulatory element binding proteins (SREBPs), which control the
 CC synthesis of fatty acids and cholesterol. The peptide derivatives of the
 CC invention are, therefore, useful in the modulation of cholesterol
 CC homeostasis and in the treatment of conditions associated with abnormal
 CC levels of plasma cholesterol, lipoproteins or triglycerides. The present
 CC sequence is a peptide substrate of S1P which can be used in a fluorogenic
 XX peptide assay of S1P
 SQ Sequence 4 AA;
 Query Match 84.2%; Score 16; DB 4; Length 4;
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RVKR 4
 DB 1 RVR 4
 RESULT 7
 AAE24432
 ID AAE24432 standard; peptide; 4 AA.
 AC AAE24432;
 XX 04-OCT-2002 (first entry)
 DT Transporter peptide, T5.
 DE Transporter peptide; therapy; colon cancer; neurodegenerative disorder;
 XX diabetes; respiratory ailment; cardioplegia; viral infection; cytostatic;
 KW virucide; neuroprotective.
 XX Unidentified.
 OS WO200231109-A2.
 PN 18-APR-2002.
 PD 15-OCT-2001; 2001WO-IB002423.
 PP 13-OCT-2000; 2000US-0240315P.
 PR (UYLA-) UNIV LAUSANNE.
 PA Bonny C;
 XX WPI; 2002-479626/51.

XX PT Novel transporter peptide useful for the intracellular delivery of
 PT biological effectors for treating diabetes, colon cancer, respiratory
 PT ailments, neurodegenerative disorders, cardioplegia, and viral infections.
 XX PS Claim 35; Page 26; 50pp; English.
 XX CC The present invention relates to novel transporter peptides with the
 CC capacity to facilitate transport of an effector across a biological
 CC membrane. Sequences of the invention are useful for translocating an
 CC effector into the cytoplasm and nucleus of a eukaryotic cell preferably a
 CC human cell. They are also useful for increasing the intracellular
 CC concentration of an effector within a eukaryotic cell, preferably human
 CC cell. Transporter peptides of the invention are useful for transporting
 CC an effector across a biological membrane, for targeting various cell
 CC types for the intracellular delivery of drugs and therapeutic agents and
 CC for increasing the biological activity of the effector to which it is
 CC coupled. Pharmaceutical compositions comprising the transporter peptides
 CC are useful for treating or preventing diseases such as colon cancer,
 CC diabetes, respiratory ailments, neurodegenerative disorders, cardioplegia
 CC and viral infections. The present sequence is a transporter peptide of
 CC the invention. This peptide can be translocated across a membrane of lung
 CC cells
 XX SQ Sequence 4 AA;

Query Match 84.2%; Score 16; DB 5; Length 4;
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RVKR 4
 ||:|
 Db 1 RVRK 4

RESULT 8
 AA014861
 ID AAO14861 standard; protein; 4 AA.

XX AC AAO14861;

XX DT 19-JUL-2002 (first entry)

XX DE Purin substrate peptide.

XX KW Furin substrate; serine protease inhibitor;
 KW serine protease substrate recognition site interaction; emphysema;
 KW respiratory distress syndrome; septic shock; multiple organ failure;
 KW myocardial ischemia; reperfusion injury; dermatitis; cystic fibrosis;
 KW chronic bronchitis; arteriosclerosis; Alzheimer's disease; corneal ulcer;
 KW rheumatoid arthritis; acute pancreatitis.

XX OS Unidentified.

XX PN US6358928-B1.

XX PD 19-MAR-2002.

XX PF 22-NOV-1999; 99US-00444883.

XX PR 22-NOV-1999; 99US-00444883.

XX PA (ENZY-) ENZYME SYST PROD INC.

XX PI Rasnick DW;

XX DR WPI; 2002-391718/42.

XX PT New alpha-amino acid or peptidyl compounds having a C-terminal
 PT imidazolesulfonylmethylene group are useful as serine protease inhibitors
 PT for treatment of e.g. Alzheimer's disease or multiple organ failure.

XX PS Claim 17; Col 11; 16pp; English.

XX CC The invention comprises alpha-amino acid and peptidyl compounds having a
 CC C-terminal imidazolesulfonylmethylene group which is a serine protease
 CC inhibitor. The compounds of the invention are capable of interacting with
 CC the substrate recognition site of a serine protease. The compounds of the
 CC invention are useful for the treatment of diseases characterised by over-
 CC activity of one or more serine proteases, e.g. respiratory distress
 CC syndrome; septic shock; multiple organ failure; emphysema; myocardial
 CC ischemia; reperfusion injury; dermatitis; cystic fibrosis; chronic
 CC bronchitis; arteriosclerosis; Alzheimer's disease; corneal ulcers;
 CC rheumatoid arthritis and acute pancreatitis. The present amino acid
 CC sequence represents the furin (serine protease) substrate peptide
 XX SQ Sequence 4 AA;

Query Match 84.2%; Score 16; DB 5; Length 4;
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RVKR 4
 ||:|
 Db 1 RVRK 4

RESULT 9
 ABP71148
 ID ABP71148 standard; peptide; 4 AA.

XX AC ABP71148;

XX DT 14-APR-2003 (first entry)

XX DE Human proneurotrophin cleavage site in BDNF protein.

XX KW Proneurotrophin; nerve growth factor; NGF; neurotrophin; NT-3; NT4; NT5;
 KW brain derived neurotrophic factor; BDNF; vasotropic; cerebroprotective;
 KW antimicrobial; cardiant; virucide; antibacterial; neuroprotective; MMP;
 KW nootropic; antiinflammatory; anticonvulsant; plasminogen; plasmin; p75;
 KW apoptosis; human.

XX OS Homo sapiens.

XX PN WO200296356-A2.

XX PD 05-DEC-2002.

XX PF 24-MAY-2002; 2002WO-US016540.

XX PR 25-MAY-2001; 2001US-0293823P.

XX PR 13-JUL-2001; 2001US-0305510P.

XX PA (CORR) CORNELL RES FOUND INC.

XX PI Hempstead BL, Lee R, Teng KK, Kermani P;

XX DR WPI; 2003-140406/13.

XX PT Novel protein for inducing apoptosis, has proneurotrophin pro-domain with
 PT conserved regions, mature neurotrophin domain, and connector that joins
 PT conserved region to mature domain and resistant to protease cleavage.

XX PS Disclosure; Page 13; 124pp; English.

XX CC The invention relates to an isolated protein comprising a pro-domain (PD)
 CC of a proneurotrophin, where PD comprises a pro-domain conserved region,
 CC or a modified proneurotrophin protein (Ib) with a PD, a mature
 CC neurotrophin domain (MD), and a connector that joins the pro-domain
 CC conserved region to MD and resistant to protease cleavage. The PD is
 CC selected from specific peptide fragments of human nerve growth factor
 CC (NGF), human brain derived neurotrophic factor (BDNF), human neurotrophin
 CC 3 (NT-3) or human neurotrophin 4/5 (NT4/5). (Ib) is useful for inducing
 CC apoptosis in a cell comprising p75 receptors (normal number or higher
 CC than the normal number of p75 receptors) on its surface, by causing the

CC p75 receptor to bind (Ib), in vitro, in mammals or humans. The method is
 CC useful for treating vascular smooth muscle plaque e.g. atherosclerotic
 CC plaque. The cell is a malignant cell e.g. cells of tumour, melanoma,
 CC prostate, pancreas, nervous system (e.g. medulloblastoma or astrocytoma),
 CC leukemia, lymphoma, testicular, lung, brain, malignant oligodendrocyte,
 CC heart, vascular smooth muscle or neural cell. A molecule that inhibits
 CC the binding of proneurotrophin to a p75 receptor is useful in a method
 CC for inhibiting apoptosis of a cell in a mammal e.g. human suffering from
 CC a condition associated with undesired apoptosis due to binding of a
 CC proneurotrophin to p75 receptor. The condition is the result of an injury
 CC or an environmental insult, e.g. nervous system injury, caused by a
 CC chemical or radiation or occurring during cancer treatment, hypoxic
 CC ischaemia caused by stroke or heart attack, viral or microbial infection,
 CC meningitis, encephalitis or abscesses, neurodegenerative disorders e.g.
 CC Alzheimer's disease, familial dysautonomia, ataxia telangiectasia,
 CC Charcot-Marie-Tooth disease, Adreno leuko dystrophy, spinal muscular
 CC atrophy or Friedreich's ataxia, or multiple sclerosis, convulsions,
 CC epilepsy and spinal cord injury. The present sequence represents the
 CC human proneurotrophin cleavage site in BDNF protein
 XX
 SQ Sequence 4 AA;

Query Match 84.2%; Score 16; DB 6; Length 4;
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVKR 4
 ||:|
 Db 1 RVRR 4

RESULT 10
 ADA10587
 ID ADA10587 standard; peptide; 4 AA.
 XX
 AC ADA10587;

DT 06-NOV-2003 (first entry)

DE Eglin c variant related fluorogenic substrate.

XX protease inhibitor; eglin c variant; reactive loop; acute bacterial;
 XX viral; fungal; infection; blocking endoproteolytic activation;
 KW bacterial toxin; anthrax toxin protective antigen; diphtheria toxin;
 KW Pseudomonas aeruginosa exotoxin A; shiga toxin; transgenic animal;
 KW fluorogenic; substrate.
 XX

OS Unidentified.

PH Key Location/Qualifiers

FT Modified-site 1 /note= "Modified by Boc"

FT Modified-site 4 /note= "Modified by MCA"

FT WO2002102318-A2.

XX 27-DEC-2002.

XX 18-JUN-2002; 2002WO-US019394.

XX 18-JUN-2001; 2001US-0299096P.

PR 17-JUN-2002; 2002US-00299096.

XX (UNMI) UNIV MICHIGAN.

XX Komiyama T, Fuller RS;

XX WPI; 2003-167438/16.

XX Composition useful for treating diseases including acute bacterial, viral
 PT and fungal infections, has protease inhibitor that is eglin c variant
 PT having a non-naturally occurring amino acid in adventitious contact site.

XX Example 1; Page 76; 112pp; English.

XX This invention relates to a novel composition comprising a protease
 PS inhibitor that is an eglin c variant comprising at least one non-
 CC naturally occurring amino acid in an adventitious contact site, and
 CC further comprising at least one non-naturally occurring amino acid in a
 CC reactive loop. The novel composition is useful for treating disease
 CC including acute bacterial (e.g. Bacillus anthracis, Corynebacterium
 CC diphtheriae, and Pseudomonas aeruginosa), viral (respiratory syncytial
 CC virus, measles virus, and human immunodeficiency virus) and fungal
 CC (candidiasis and pneumocystis pneumonia) infections in a patient exposed
 CC to an infectious agent. The eglin c variants are useful for blocking
 CC endoproteolytic activation of a bacterial toxin including anthrax toxin A
 CC protective antigen, diphtheria toxin, Pseudomonas aeruginosa exotoxin A
 CC and shiga toxin. The eglin c variants are also useful as affinity
 CC purification reagents, as fluorescence tags for identification of cells
 CC and for tracking internalisation of drugs and for examining and
 CC inhibiting physiological functions of processing or other proteases in
 CC cell cultures or in transgenic animals, for example by selectively
 CC inhibiting the enzymes. The eglin c variants are small, stable and
 CC reversible. This sequence represents a fluorescent substrate peptide used
 CC in the creation of first generation eglin c variants of the invention.
 XX
 SQ Sequence 4 AA;

Query Match 84.2%; Score 16; DB 6; Length 4;
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVKR 4
 ||:|
 Db 1 RVRR 4

RESULT 11
 ADD84924

ID ADD84924 standard; peptide; 4 AA.

XX
 AC ADD84924;

XX 29-JAN-2004 (first entry)

DT Tetrapeptide protease-sensitive linker SEQ ID NO:19.

DE molecular adjuvant; nicotine hapten; antiaddictive; vaccine; nicotine;
 XX smoking; nicotine addiction; immunisation.

OS Synthetic.

XX WO2003082329-A2.

XX 09-OCT-2003.

XX 20-FEB-2003; 2003WO-US005015.

XX 01-MAR-2002; 2002US-0360967P.

XX (UYNE-) UNIV NEBRASKA.
 PA (SAND/) SANDERSON S D G.
 PA (VENN/) VENNSTROM J L.
 PA (THIE/) THIELE G M.
 PA (PARA/) PARAMESWARAN M.
 PA (BEVI/) BEVINS R A.
 PA (SRIN/) SRINIVASA C R.

XX Sanderson SDG, Vennstrom JL, Thiele GM, Parameswaran M;
 PI Bevins RA, Srinivasa CR;

XX WPI; 2003-902908/82.

XX Compound useful as nicotine vaccine comprises molecular adjuvant with

PT targeting ligand linked to nicotine hapten.

PS Example 5; SEQ ID NO 19; 90pp; English.

XX

CC The present invention describes a compound (I) comprising a molecular

CC adjuvant linked to a nicotine hapten. The molecular adjuvant comprises a

CC targeting ligand having binding affinity for an antigen presenting cell.

CC The targeting ligand is functionally linked to the nicotine hapten so

CC that the binding of the molecular adjuvant to the antigen presenting cell

CC determinant activates the antigen presenting cell and effecting delivery

CC of the nicotine hapten to an antigen presenting pathway. Also described

CC is a method for the preparation of antibodies to a nicotine hapten

CC involving: (a) immunising an animal with (I); (b) isolating antibodies

CC from the sera of the animal; and (c) recovering the isolated antibodies.

CC (I) has antiaddictive activities, and can be used in vaccines. (I) can be

CC used for the treatment or prevention of nicotine addiction via

CC immunisation with a nicotine vaccine. The compound (I) is capable of

CC causing smoking cessation and long term compliance; and delivers both

CC stimulatory signals and the nicotine antigen to antigen presenting cells

CC (APCs), and so inducing an anti-nicotine antibody response with little or

CC no inflammatory side effects and without reliance on other added

CC adjuvants. The present sequence is used in the exemplification of the

CC present invention.

XX

SQ Sequence 4 AA;

Query Match 84.2%; Score 16; DB 7; Length 4;

Best Local Similarity 75.0%; Pred. NO. 1.8e+06;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVKR 4

DB ||:|

1 RVRR 4

RESULT 12

ADG19004

ID ADG19004 standard; peptide; 4 AA.

XX

AC ADG19004;

DT 11-MAR-2004 (first entry)

XX

DE Multimeric transporter peptide related peptide SEQ ID NO:29.

XX

KW multimetric transporter peptide; transporter peptide; antidiabetic;

KW cytostatic; antiinflammatory; nontropic; neuroprotective; virucide;

KW gene therapy; diabetes; colon cancer; respiratory ailment;

KW neurodegenerative disorder; cardioplegia; viral infection.

XX

OS Synthetic.

XX

PN WO2003103718-A2.

XX

PD 18-DEC-2003.

XX

XX 06-JUN-2003; 2003WO-IB003097.

PF

XX 07-JUN-2002; 2002US-00165015.

PR

XX (UYLA-) UNIV LAUSANNE.

PA

PI Bonny C;

XX

DR WPI; 2004-062229/06.

XX

XX New multimeric transporter peptides, useful for treating diabetes, colon

PT cancer, respiratory ailments, neurodegenerative disorders, cardioplegia,

PT and viral infections.

XX

PS Claim 3; SEQ ID NO 29; 49pp; English.

XX

CC The present invention describes a multimeric transporter peptide (I).

CC

CC Also described: (1) a transporter unit comprising the transporter peptide

CC and an effector; (2) translocating the transporter unit across the

CC membrane of pancreatic beta-cells, hepatocytes, muscle cells or lung

CC cells; (3) a pharmaceutical composition comprising the transporter unit

CC and a carrier; (4) a method of producing a translocatable conjugate

CC between the transporter peptide and an effector; (5) a method of

CC increasing the intracellular concentration of an effector with a

CC eukaryotic cell; (6) a kit comprising in one or more containers, the

CC pharmaceutical composition described above; and (7) a method of treating

CC or preventing a disease. (I) has antidiabetic, cytostatic,

CC antiinflammatory, nontropic, neuroprotective and virucide activities, and

CC can be used in gene therapy. The multimeric transporter peptide (I),

CC compositions and methods of the present invention can be used for

CC treating diabetes, colon cancer, respiratory ailments, neurodegenerative

CC disorders, cardioplegia, and viral infections. The present sequence

CC represents a peptide which can be used as part of a multimeric

CC transporter peptide of the present invention.

XX

SQ Sequence 4 AA;

Query Match 84.2%; Score 16; DB 8; Length 4;

Best Local Similarity 75.0%; Pred. NO. 1.8e+06;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVKR 4

DB ||:|

1 RVRR 4

RESULT 13

ADJ57390

ID ADJ57390 standard; peptide; 4 AA.

XX

AC ADJ57390;

XX

DT 06-MAY-2004 (first entry)

XX

DE Peptide fragment of alpha-1-antitrypsin, use as convertase inhibitor.

XX

KW Convertase; inhibitor; alpha-1-antitrypsin; antiinflammatory; vulnery;

KW ophthalmological; dermatological; nephrotropic; hepatotropic; vasotropic;

KW antiinfertility; respiratory-gen.; cardiant; CNS-gen.; cerebroprotective;

KW neuroprotective; nontropic; cytostatic; antiarthritic;

KW antiarteriosclerotic.

XX

OS Unidentified.

XX

PN WO2004009113-A1.

XX

PD 29-JAN-2004.

XX

XX 23-JUL-2003; 2003WO-GB003159.

PF

XX 24-JUL-2002; 2002GB-00017136.

PR

XX (RENO-) RENOVO LTD.

PA

PI Ferguson MWJ, Brunner G;

XX

XX WPI; 2004-180270/17.

DR

XX

PT Use of a convertase inhibitor in the manufacture of a medicament for

PT reducing scarring during the healing of wounds or reducing fibrosis in

PT the treatment of fibrotic conditions.

XX

PS Disclosure; Page 10; 43pp; English.

XX

CC The present sequence is that of a peptide fragment of alpha-1-

CC antitrypsin. Convertase inhibitors of the invention may be derivatives of

CC alpha-1-antitrypsin comprising this sequence. The inventors have

CC established that convertase enzymes act, both extracellularly and

CC intracellularly, to cause the activation of latent transforming growth

CC factor-beta (TGF-beta) in the extracellular space at the site of a wound

CC of a fibrotic conditions. Thus, the present invention relates to use of
 CC convertase inhibitors for the reduction of scarring during the healing of
 CC wounds, for reducing fibrosis in the treatment of fibrotic conditions,
 CC for treating wounds to prevent scar formation, for preventing scarring of
 CC the eye, nervous tissue or intestines, dermal scarring and scarring
 CC following a burn. The fibrotic condition is a fibrotic disorder such as
 CC glomerulonephritis, cirrhosis of the liver, fibrotic disease, adhesions
 CC and restenosis (all claimed). The convertase inhibitor can also be used
 CC for the treatment of hypertrophic and keloid scars, scarring in the heart,
 CC scarring of the gut, scarring in the pelvis in the region of the
 CC fallopian tubes leading to infertility, scarring following injury to the
 CC muscles, scarring or fibrosis following injury to tendons and ligaments,
 CC which can result in serious loss of function, liver fibrosis, pulmonary
 CC fibrosis, scleroderma, myocardial hibernation, fibrosis following a
 CC myocardial infarction, central nervous system fibrosis following a stroke
 CC or neurodegenerative disorders (e.g. Alzheimer's disease), proliferative
 CC vitreoretinopathy, arthritis, arteriosclerosis and cancer.
 XX
 SQ Sequence 4 AA;

Query Match 84.2%; Score 16; DB 8; Length 4;
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVKR 4
 ||:
 Db 1 RVKR 4

RESULT 14

CC AAR37629
 ID AAR37629 standard; protein; 4 AA.
 XX
 AC AAR37629;
 XX
 DT 25-MAR-2003 (revised)
 DT 24-SEP-1993 (first entry)
 XX
 DE Sequence of proinsulin variant proins.RTKR.Ip having a non-naturally
 DE occurring prohormone convertase cleavage site.

XX Prohormone convertase; enzyme; cleavage; proinsulin; hormone.

XX Synthetic.

XX WO9311247-A1.

XX 10-JUN-1993.

XX 04-DEC-1992; 92WO-US010621.

XX 06-DEC-1991; 91US-00803631.

XX 22-MAY-1992; 92US-00887265.

XX (GETH) GENENTECH INC.

XX Gorman CM, Groskreutz DJ, Marriott D;

XX WPI; 1993-197065/24.

XX Heterologous polypeptide factor prepn. - by introducing into polypeptide
 PT factor dependent host cell nucleic acid, and then culturing host cell,
 PT etc.

XX Example; Page 56; 134pp; English.

XX The inventors describe the production of mammalian cells expressing
 CC prohormone convertase which facilitates the processing of prohormone
 CC precursors to active hormones. More specifically the cleavage site is the
 CC prohormone convertase cleavage site given in AAR37632-35. A human
 CC proinsulin mutant having a non-naturally occurring prohormone convertase
 CC cleavage site is constructed by mutating the human proinsulin cDNA,
 CC pRK.proins encoding the naturally occurring basic cleavage site at the B-

CC chain/C-peptide junction (AAR37627) and/or A-chain/C-peptide junction
 CC (AAR37628) by site-directed mutagenesis (Kunkel 1987). The following
 CC proinsulin variants were constructed: proins.RTKR.Ip, proins.RQKR.IIp and
 CC proins.KTKR.Ip (see AAR37629-31). The following double proinsulin
 CC variants were constructed: proins.KR.Ip/RQKR.IIp and
 CC proins.RTKR.Ip/RQKR.IIp. Primers used in proinsulin mutant construction
 CC were AAQ43265-67. (Updated on 25-MAR-2003 to correct PN field.)
 XX

SQ Sequence 4 AA;

Query Match 78.9%; Score 15; DB 2; Length 4;
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RVKR 4
 ||:
 Db 1 RVKR 4

RESULT 15

CC AAR60593
 ID AAR60593 standard; peptide; 4 AA.

XX AAR60593;

XX 25-MAR-2003 (revised)

DT 27-APR-1995 (first entry)

DE proins.RTKR.Ip proinsulin mutant cleavage site.

XX prohormone; convertase; insulin; proinsulin; proproinsulin; factor;

KW growth; precursors; transgenic; mammal; pcr; primer.

XX Synthetic.

XX WO9420624-A1.

XX 15-SEP-1994.

XX 01-MAR-1994; 94WO-US002233.

XX 01-MAR-1993; 93US-00026143.

XX (GETH) GENENTECH INC.

XX Gorman CM, Groskreutz DJ;

XX WPI; 1994-303031/37.

XX Treating insulin-dependent disorders in mammals - by introducing a
 PT nucleic acid encoding a variant proinsulin into a host cell with a
 PT constitutive pathway of protein secretion, or a plasmid, and introducing
 PT the cell or plasmid to the mammal.

XX Example 4; Page 54; 117pp; English.

XX The cDNA clone of the human proinsulin gene, pSVEHIGDHP, was
 CC amplified by primers AAQ71463-4 in a RACE-PCR. The product was ligated in
 CC plasmid pRK5 and called pRK.proins. Mutants of the prohormone convertase
 CC (PC) cleavage site in the human proinsulin were constructed (AAR60591-
 CC 5) The mutated sites are specifically recognised by murine PC. The new
 CC cleavage sites are labelled either Ip or Iip. Ip is a Type I enzyme
 CC cleavage site whereas Iip is a Type II enzyme cleavage site. Cells
 CC containing both the prohormone convertase gene and the required precursor
 CC gene e.g proproinsulin to be expressed can be injected into a mammal.
 CC This system can be used to treat insulin-responsive disorders. (Updated
 CC on 25-MAR-2003 to correct PN field.)
 XX

SQ Sequence 4 AA;

Query Match 78.9%; Score 15; DB 2; Length 4;
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 RVKR 4
| |
Db 1 RTRK 4

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OM protein - protein search, using sw model

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Perfect score: 19

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Scoring table: BLOSUM62

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Searched: 513545 seqs, 74649064 residues

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Maximum Match 100%

Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	16	84.2	4	1	US-08-398-028B-73
5	16	84.2	4	2	US-08-504-265B-73
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7	16	84.2	4	3	US-08-481-534-20
8	16	84.2	4	3	US-08-753-247-29
9	16	84.2	4	3	US-09-360-237-40
10	16	84.2	4	3	US-09-360-237-54
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12	16	84.2	4	4	US-09-640-198D-33
13	16	84.2	4	4	US-09-639-667-3
14	15	78.9	4	1	US-08-200-900A-36
15	15	78.9	4	1	US-08-200-900A-38
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17	15	78.9	4	2	US-08-545-562A-65
18	15	78.9	4	3	US-08-026-143B-22
19	15	78.9	4	3	US-09-537-696-23
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25	15	78.9	4	5	PCT-US94-02233-22
26	15	78.9	4	5	PCT-US94-07779-16
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28	14	73.7	4	2	US-08-595-043A-15	Sequence 15, Appl
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32	14	73.7	4	3	US-09-391-104-33	Sequence 33, Appl
33	14	73.7	4	4	US-09-185-852-11	Sequence 11, Appl
34	14	73.7	4	4	US-09-640-198D-7	Sequence 7, Appl
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63	13	68.4	4	3	US-08-641-873-13	Sequence 13, Appl
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65	13	68.4	4	3	US-08-472-240A-21	Sequence 21, Appl
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99	11	57.9	4	1	US-08-808-641-13	Sequence 13, Appl
100	11	57.9	4	2	US-08-025-321C-11	Sequence 11, Appl

ALIGNMENTS

```
RESULT 1
US-08-002-202-4
; Sequence 4, Application US/08002202
; Patent No. 5604201
; GENERAL INFORMATION:
; APPLICANT: Thomas, Garry
; APPLICANT: Anderson, Eric D
; APPLICANT: Thomas, Laurel
; APPLICANT: Hayflick, Joel S
; TITLE OF INVENTION: Methods and Reagents for Inhibiting
; TITLE OF INVENTION: Purin Endoprotease
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti and Witcoff, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 08-JAN-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5604201nan, Kevin E
; REGISTRATION NUMBER: 35,30003
; REFERENCE/DOCKET NUMBER: 92,448
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1..4
; OTHER INFORMATION: /label= Modified-sites
; OTHER INFORMATION: /note= "The amino terminus is derivatized by a
; OTHER INFORMATION: butoxycarbonyl group, and the carboxyl terminus is
; OTHER INFORMATION: derivatized by a 4-methylcoumaryl-7-amide group;"
; US-08-002-202-4

Query Match 84.2%; Score 16; DB 1; Length 4;
Best Local Similarity 75.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVKR 4
Db 1 RVRR 4

RESULT 2
US-08-002-202-20
; Sequence 20, Application US/08002202
; Patent No. 5604201
; GENERAL INFORMATION:
; APPLICANT: Thomas, Garry
; APPLICANT: Anderson, Eric D
; APPLICANT: Thomas, Laurel
; APPLICANT: Hayflick, Joel S
; TITLE OF INVENTION: Methods and Reagents for Inhibiting
; TITLE OF INVENTION: Purin Endoprotease
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti and Witcoff, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
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; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/002,202
; FILING DATE: 08-JAN-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5604201nan, Kevin E
; REGISTRATION NUMBER: 35,30003
; REFERENCE/DOCKET NUMBER: 92,448
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1..4
; OTHER INFORMATION: /label= Modified-sites
; OTHER INFORMATION: /note= "The amino terminus is derivatized by a
; OTHER INFORMATION: butoxycarbonyl group, and the carboxyl terminus is
; OTHER INFORMATION: derivatized by a 4-methylcoumaryl-7-amide group;"
; US-08-002-202-20

Query Match 84.2%; Score 16; DB 1; Length 4;
Best Local Similarity 75.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVKR 4
Db 1 RVRR 4

RESULT 3
US-08-460-343B-73
; Sequence 73, Application US/08460343B
; Patent No. 5741664
; GENERAL INFORMATION:
; APPLICANT: Marcus D. Ballinger and James A. Wells
; TITLE OF INVENTION: SUBSTITUTED VARIANTS CAPABLE OF CLEAVING
; TITLE OF INVENTION: SUBSTRATES CONTAINING DIBASIC RESIDUES
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,343B
; FILING DATE: 01-Jun-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/398028
; FILING DATE: 03-mar-1995
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; ATTORNEY/AGENT INFORMATION:
; NAME: Kubinec, Jeffrey S.
; REGISTRATION NUMBER: 36,575
; REFERENCE/DOCKET NUMBER: P0936C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/952-8228
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-460-343B-73

Query Match      84.2%; Score 16; DB 1; Length 4;
Best Local Similarity 75.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RVKR 4
Db      1 RVRR 4

RESULT 4
US-08-398-028B-73
; Sequence 73, Application US/08398028B
; Patent No. 5780285
; GENERAL INFORMATION:
; APPLICANT: Marcus D. Ballinger and James A. Wells
; TITLE OF INVENTION: SUBSTITUTED VARIANTS CAPABLE OF CLEAVING
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/398,028B
; FILING DATE: 03-Mar-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/398028
; FILING DATE: 03-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Kubinec, Jeffrey S.
; REGISTRATION NUMBER: 36,575
; REFERENCE/DOCKET NUMBER: P0936P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8228
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-504-265B-73

Query Match      84.2%; Score 16; DB 2; Length 4;
Best Local Similarity 75.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RVKR 4
Db      1 RVRR 4

RESULT 6
US-08-481-534-4
; Sequence 4, Application US/08481534
; Patent No. 6022855
; GENERAL INFORMATION:
; APPLICANT: Thomas, Gary
; APPLICANT: Anderson, Eric D
; APPLICANT: Thomas, Laurel
; APPLICANT: Haylick, Joel S
; APPLICANT: Nelson, Jay
; APPLICANT: Stenglen, Stephan G
; TITLE OF INVENTION: Methods and reagents for inhibiting furin
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESS: McDonnell Boehrnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/481,534
/ FILING DATE: 14-SEP-1995
/ CLASSIFICATION: 530
/ ATTORNEY/AGENT INFORMATION:
/ NAME: No. 6022855nan, Kevin E
/ REGISTRATION NUMBER: 35,303
/ REFERENCE/DOCKET NUMBER: 92,448-D
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-913-0001
/ TELEFAX: 312-913-0002
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 4 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-08-481-534-4

Query Match      84.2%; Score 16; DB 3; Length 4;
Best Local Similarity 75.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RVKR 4
Db      1 RVRR 4

RESULT 7
US-08-481-534-20
/ Sequence 20, Application US/08481534
/ Patent No. 6022855
/ GENERAL INFORMATION:
/ APPLICANT: Thomas, Gary
/ APPLICANT: Anderson, Eric D
/ APPLICANT: Thomas, Laurel
/ APPLICANT: Haylick, Joel S
/ APPLICANT: Nelson, Jay
/ APPLICANT: Stenglen, Stephan G
/ TITLE OF INVENTION: Methods and Reagents for Inhibiting Furin
/ TITLE OF INVENTION: Endoprotease
/ NUMBER OF SEQUENCES: 21
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
/ STREET: 300 South Wacker Drive
/ CITY: Chicago
/ STATE: IL
/ COUNTRY: USA
/ ZIP: 60606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/481,534
/ FILING DATE: 14-SEP-1995
/ CLASSIFICATION: 530
/ ATTORNEY/AGENT INFORMATION:
/ NAME: No. 6022855nan, Kevin E
/ REGISTRATION NUMBER: 35,303
/ REFERENCE/DOCKET NUMBER: 92,448-D
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-913-0001
/ TELEFAX: 312-913-0002
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 20:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 4 amino acids
/ TYPE: amino acid
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/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ FEATURE:
/ NAME/KEY: Modified site
/ LOCATION: 1..4
/ OTHER INFORMATION: /label=Modified site
/ OTHER INFORMATION: /note="The amino terminus us derivatized by a
/ OTHER INFORMATION: butoxycarbonyl group, and the carboxyl terminus
/ OTHER INFORMATION: is derivatized by a 4-methylcoumaryl-7-amide group."
/ US-08-481-534-20

Query Match      84.2%; Score 16; DB 3; Length 4;
Best Local Similarity 75.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RVKR 4
Db      1 RVRR 4

RESULT 8
US-08-753-247-29
/ Sequence 29, Application US/08753247
/ Patent No. 6210929
/ GENERAL INFORMATION:
/ APPLICANT: SCHLOKAT, Uwe
/ APPLICANT: FISCHER, Bernhard
/ APPLICANT: FALKNER, Falko-Guenther
/ APPLICANT: DORNER, Friedrich
/ APPLICANT: EIBL, Johann
/ TITLE OF INVENTION: A FUSION PROTEIN COMPRISING A FURIN
/ TITLE OF INVENTION: DERIVATIVE OR A DERIVATIVE OF A FURIN ANALOGUE AND A
/ NUMBER OF SEQUENCES: 29
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Foley & Lardner
/ STREET: 3000 K Street, N.W., Suite 500
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20007-5109
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/753,247
/ FILING DATE: 22-NOV-1996
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: AT 1928/95
/ FILING DATE: 24-NOV-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: BENT, Stephen A.
/ REGISTRATION NUMBER: 29,768
/ REFERENCE/DOCKET NUMBER: 40433/149
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202)672-5300
/ TELEFAX: (202)672-5399
/ TELEX: 904136
/ INFORMATION FOR SEQ ID NO: 29:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 4 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-753-247-29

Query Match      84.2%; Score 16; DB 3; Length 4;
Best Local Similarity 75.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY      1 RVKR 4
      ||:|
Db      1 RVRR 4

RESULT 9
US-09-360-237-40
; Sequence 40, Application US/09360237
; Patent No. 6322962
; GENERAL INFORMATION:
; APPLICANT: BROWN, MICHAEL S.
; APPLICANT: CHENG, DONG
; APPLICANT: ESPENSHADE, PETER J.
; APPLICANT: GOLDSTEIN, JOSEPH L.
; APPLICANT: RAWSON, ROBERT B.
; APPLICANT: SAKAI, JURO
; TITLE OF INVENTION: STEROL-REGULATED SITE-1 PROTEASE AND ASSAYS OF
; TITLE OF INVENTION: MODULATORS THEREOF
; FILE REFERENCE: UTXD:567
; CURRENT APPLICATION NUMBER: US/09/360,237
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: 60/096,571
; EARLIER FILING DATE: 1998-08-14
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
; OTHER INFORMATION: PEPTIDE
US-09-360-237-40

Query Match      84.2%; Score 16; DB 3; Length 4;
Best Local Similarity 75.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RVKR 4
      ||:|
Db      1 RVRR 4

RESULT 10
US-09-360-237-54
; Sequence 54, Application US/09360237
; Patent No. 6322962
; GENERAL INFORMATION:
; APPLICANT: BROWN, MICHAEL S.
; APPLICANT: CHENG, DONG
; APPLICANT: ESPENSHADE, PETER J.
; APPLICANT: GOLDSTEIN, JOSEPH L.
; APPLICANT: RAWSON, ROBERT B.
; APPLICANT: SAKAI, JURO
; TITLE OF INVENTION: STEROL-REGULATED SITE-1 PROTEASE AND ASSAYS OF
; TITLE OF INVENTION: MODULATORS THEREOF
; FILE REFERENCE: UTXD:567
; CURRENT APPLICATION NUMBER: US/09/360,237
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: 60/096,571
; EARLIER FILING DATE: 1998-08-14
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 54
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
; OTHER INFORMATION: PEPTIDE
US-09-360-237-54

Query Match      84.2%; Score 16; DB 3; Length 4;
Best Local Similarity 75.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RVKR 4
      ||:|
Db      1 RVRR 4

RESULT 11
US-09-444-883-3
; Sequence 3, Application US/09444883
; Patent No. 6358928
; GENERAL INFORMATION:
; APPLICANT: RASNICK, DAVID W.
; TITLE OF INVENTION: PEPTIDYL SULFONYL IMIDAZOLIDES AS SELECTIVE INHIBITORS OF
; TITLE OF INVENTION: SERINE PROTEASES
; FILE REFERENCE: 6095-5
; CURRENT APPLICATION NUMBER: US/09/444,883
; CURRENT FILING DATE: 1999-11-22
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Binding Site for Furin
; OTHER INFORMATION: 883-3
US-09-444-883-3

Query Match      84.2%; Score 16; DB 3; Length 4;
Best Local Similarity 75.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RVKR 4
      ||:|
Db      1 RVRR 4

RESULT 12
US-09-640-198D-33
; Sequence 33, Application US/09640198D
; Patent No. 6586411
; GENERAL INFORMATION:
; APPLICANT: RUSSELL, STEPHEN
; APPLICANT: KAY WHYE, PENG
; TITLE OF INVENTION: System for Monitoring the Location of
; TITLE OF INVENTION: Transgenes
; FILE REFERENCE: 07039-295001
; CURRENT APPLICATION NUMBER: US/09/640,198D
; CURRENT FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: US 60/149,168
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Cleavable Linker Site
; OTHER INFORMATION: 198D-33
US-09-640-198D-33

Query Match      84.2%; Score 16; DB 4; Length 4;
Best Local Similarity 75.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RVKR 4
      ||:|
Db      1 RLKR 4

RESULT 13
US-09-639-667-3
; Sequence 3, Application US/09639667
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/ Patent No. 6632800
/ GENERAL INFORMATION:
/ APPLICANT: Russell, Stephen James
/ APPLICANT: Peng, Kan Whye
/ TITLE OF INVENTION: SYSTEM FOR MONITORING THE EXPRESSION OF
/ FILE REFERENCE: 07039-292001
/ CURRENT APPLICATION NUMBER: US/09/639,667
/ CURRENT FILING DATE: 2001-06-04
/ PRIOR APPLICATION NUMBER: 60/149,168
/ PRIOR FILING DATE: 1999-08-17
/ NUMBER OF SEQ ID NOS: 31
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 3
/ LENGTH: 4
/ TYPE: PRT
/ ORGANISM: Unknown
/ FEATURE:
/ OTHER INFORMATION: linker peptide
US-09-639-667-3

Query Match 84.2%; Score 16; DB 4; Length 4;
Best Local Similarity 75.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVKR 4
|:|
Db 1 RLKR 4

RESULT 14
US-08-200-900A-36
/ Sequence 36, Application US/08200900A
/ Patent No. 5665566
/ GENERAL INFORMATION:
/ APPLICANT:
/ TITLE OF INVENTION: CLONING OF ENTEROKINASE AND METHOD OF USE
/ NUMBER OF SEQUENCES: 38
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Genetics Institute, Inc. - Legal Affairs
/ STREET: 87 CambridgePark Drive
/ CITY: Cambridge
/ STATE: MA
/ COUNTRY: USA
/ ZIP: 02140
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/200,900A
/ FILING DATE: 23-FEB-1994
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Meinert, Maureen C.
/ REGISTRATION NUMBER: 31,544
/ REFERENCE/DOCKET NUMBER: GI 5201-FWC
/ TELEPHONE: (617) 876-1170 X8574
/ TELEFAX: (617) 876-5851
/ INFORMATION FOR SEQ ID NO: 36:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 4 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-200-900A-36

Query Match 78.9%; Score 15; DB 1; Length 4;
Best Local Similarity 75.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RVKR 4
|:|
Db 1 RTKR 4

RESULT 15
US-08-200-900A-38
/ Sequence 38, Application US/08200900A
/ Patent No. 5665566
/ GENERAL INFORMATION:
/ APPLICANT:
/ TITLE OF INVENTION: CLONING OF ENTEROKINASE AND METHOD OF USE
/ NUMBER OF SEQUENCES: 38
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Genetics Institute, Inc. - Legal Affairs
/ STREET: 87 CambridgePark Drive
/ CITY: Cambridge
/ STATE: MA
/ COUNTRY: USA
/ ZIP: 02140
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/200,900A
/ FILING DATE: 23-FEB-1994
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Meinert, Maureen C.
/ REGISTRATION NUMBER: 31,544
/ REFERENCE/DOCKET NUMBER: GI 5201-FWC
/ TELEPHONE: (617) 876-1170 X8574
/ TELEFAX: (617) 876-5851
/ INFORMATION FOR SEQ ID NO: 38:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 4 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-200-900A-38

Query Match 78.9%; Score 15; DB 1; Length 4;
Best Local Similarity 75.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RVKR 4
|:|
Db 1 RTKR 4

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Job time : 30 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

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(without alignments)
14.768 Million cell updates/sec

Title: US-09-885-914B-3

Perfect score: 19

Sequence: 1 RVKR 4

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
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- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	100.0	4	11	US-09-885-914B-3
2	19	100.0	4	16	US-10-478-179-8
3	16	84.2	4	9	US-09-977-831-29
4	16	84.2	4	14	US-10-165-015-29
5	16	84.2	4	14	US-10-155-886-24
6	16	84.2	4	15	US-10-428-868-33
7	16	84.2	4	16	US-10-399-127-29
8	16	84.2	4	16	US-10-641-834-3
9	15	78.9	4	9	US-09-887-669-12
10	15	78.9	4	9	US-09-841-730-23
11	15	78.9	4	10	US-09-997-868-22
					Sequence 3, Appli
					Sequence 8, Appli
					Sequence 29, Appli
					Sequence 24, Appli
					Sequence 33, Appli
					Sequence 29, Appli
					Sequence 3, Appli
					Sequence 12, Appli
					Sequence 23, Appli
					Sequence 22, Appli

12	15	78.9	4	13	US-10-013-032-23	Sequence 23, Appli
13	15	78.9	4	13	US-10-074-956-26	Sequence 26, Appli
14	15	78.9	4	15	US-10-115-134-60	Sequence 60, Appli
15	15	78.9	4	17	US-10-831-302-15	Sequence 15, Appli
16	15	78.9	4	17	US-10-831-304-38	Sequence 38, Appli
17	15	78.9	4	17	US-10-942-581-5	Sequence 5, Appli
18	14	73.7	4	9	US-09-734-002-14	Sequence 14, Appli
19	14	73.7	4	9	US-09-391-104-33	Sequence 33, Appli
20	14	73.7	4	9	US-09-813-653-11	Sequence 11, Appli
21	14	73.7	4	14	US-10-328-813-11	Sequence 11, Appli
22	14	73.7	4	14	US-10-045-612A-23	Sequence 23, Appli
23	14	73.7	4	15	US-10-057-620-17	Sequence 17, Appli
24	14	73.7	4	15	US-10-428-868-7	Sequence 7, Appli
25	14	73.7	4	15	US-10-215-272-34	Sequence 34, Appli
26	14	73.7	4	16	US-10-716-326-34	Sequence 34, Appli
27	14	73.7	4	16	US-10-641-834-5	Sequence 5, Appli
28	14	73.7	4	17	US-10-715-976-34	Sequence 34, Appli
29	13	68.4	4	9	US-09-391-104-9	Sequence 9, Appli
30	13	68.4	4	9	US-09-006-298-28	Sequence 28, Appli
31	13	68.4	4	9	US-09-977-831-16	Sequence 16, Appli
32	13	68.4	4	9	US-09-874-736-7	Sequence 7, Appli
33	13	68.4	4	10	US-09-997-868-23	Sequence 23, Appli
34	13	68.4	4	13	US-10-002-278-17	Sequence 17, Appli
35	13	68.4	4	13	US-10-003-035-11	Sequence 11, Appli
36	13	68.4	4	13	US-10-013-032-19	Sequence 19, Appli
37	13	68.4	4	13	US-10-061-395-43	Sequence 43, Appli
38	13	68.4	4	14	US-10-165-015-16	Sequence 16, Appli
39	13	68.4	4	14	US-10-155-886-23	Sequence 23, Appli
40	13	68.4	4	14	US-10-052-942-49	Sequence 49, Appli
41	13	68.4	4	14	US-10-286-332A-11	Sequence 11, Appli
42	13	68.4	4	14	US-10-358-627-11	Sequence 11, Appli
43	13	68.4	4	14	US-10-358-627-16	Sequence 16, Appli
44	13	68.4	4	15	US-10-280-915-11	Sequence 11, Appli
45	13	68.4	4	15	US-10-387-336-23	Sequence 23, Appli
46	13	68.4	4	15	US-10-057-620-10	Sequence 10, Appli
47	13	68.4	4	15	US-10-215-272-38	Sequence 38, Appli
48	13	68.4	4	16	US-10-726-422-7	Sequence 7, Appli
49	13	68.4	4	16	US-10-399-127-16	Sequence 16, Appli
50	13	68.4	4	16	US-10-471-220-27	Sequence 27, Appli
51	13	68.4	4	16	US-10-716-326-38	Sequence 38, Appli
52	13	68.4	4	16	US-10-286-332A-11	Sequence 11, Appli
53	13	68.4	4	16	US-10-280-915-11	Sequence 11, Appli
54	13	68.4	4	17	US-10-808-187-1178	Sequence 1178, Ap
55	13	68.4	4	17	US-10-868-381-19	Sequence 19, Appli
56	13	68.4	4	17	US-10-823-259-17	Sequence 17, Appli
57	13	68.4	4	17	US-10-823-254-17	Sequence 17, Appli
58	13	68.4	4	17	US-10-506-651-30	Sequence 30, Appli
59	13	68.4	4	17	US-10-715-976-38	Sequence 38, Appli
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62	12	63.2	4	10	US-09-997-868-24	Sequence 24, Appli
63	12	63.2	4	11	US-09-882-781-22	Sequence 22, Appli
64	12	63.2	4	11	US-09-885-914B-2	Sequence 2, Appli
65	12	63.2	4	14	US-10-155-886-25	Sequence 25, Appli
66	12	63.2	4	14	US-10-005-931-22	Sequence 22, Appli
67	12	63.2	4	15	US-10-612-090-5	Sequence 5, Appli
68	12	63.2	4	16	US-10-432-234A-564	Sequence 564, App
69	12	63.2	4	16	US-10-723-933-17	Sequence 17, Appli
70	12	63.2	4	16	US-10-723-933-105	Sequence 105, App
71	12	63.2	4	17	US-10-863-040-149	Sequence 149, App
72	12	63.2	4	19	US-11-016-922-23	Sequence 23, Appli
73	11	57.9	4	10	US-09-852-910-153	Sequence 26, Appli
74	11	57.9	4	14	US-10-261-894-26	Sequence 3, Appli
75	11	57.9	4	15	US-10-197-000-3	Sequence 18, Appli
76	11	57.9	4	15	US-10-057-620-18	Sequence 3, Appli
77	11	57.9	4	15	US-10-245-871-3	Sequence 8, Appli
78	11	57.9	4	15	US-10-245-871-8	Sequence 8, Appli
79	11	57.9	4	15	US-10-245-871-801	Sequence 801, App
80	11	57.9	4	15	US-10-215-272-35	Sequence 35, Appli
81	11	57.9	4	15	US-10-411-336A-153	Sequence 153, App
82	11	57.9	4	15	US-10-253-286-3	Sequence 3, Appli
83	11	57.9	4	15	US-10-253-286-8	Sequence 8, Appli
84	11	57.9	4	15	US-10-253-286-801	Sequence 801, App

85 11 57.9 4 16 US-10-751-699-82 Sequence 82, Appl
86 11 57.9 4 16 US-10-716-326-35 Sequence 35, Appl
87 11 57.9 4 16 US-10-785-230-10 Sequence 10, Appl
88 11 57.9 4 16 US-10-841-787-1 Sequence 1, Appl
89 11 57.9 4 16 US-10-841-787-3 Sequence 3, Appl
90 11 57.9 4 16 US-10-795-676-63 Sequence 63, Appl
91 11 57.9 4 16 US-10-841-056-12 Sequence 12, Appl
92 11 57.9 4 16 US-10-841-121-12 Sequence 12, Appl
93 11 57.9 4 17 US-10-433-709-12 Sequence 12, Appl
94 11 57.9 4 17 US-10-715-976-35 Sequence 35, Appl
95 10 52.6 2 18 US-10-503-910-38 Sequence 38, Appl
96 10 52.6 3 10 US-09-852-910-154 Sequence 154, App
97 10 52.6 3 14 US-10-227-110-18 Sequence 18, Appl
98 10 52.6 3 14 US-10-208-508-18 Sequence 18, Appl
99 10 52.6 3 15 US-10-411-336A-154 Sequence 154, App
100 10 52.6 3 15 US-10-363-112-56 Sequence 56, Appl

ALIGNMENTS

RESULT 1
US-09-885-914B-3
; Sequence 3, Application US/09885914B
; Publication No. US20040127396A1
; GENERAL INFORMATION:
; APPLICANT: DUBOIS, Claire
; TITLE OF INVENTION: USE OF FURIN AND FURIN-LIKE PROTEASE INHIBITORS IN THE TREATMENT
; FILE OF INVENTION: 85761-28
; FILE REFERENCE: 85761-28
; CURRENT APPLICATION NUMBER: US/09/885,914B
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/213,995
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: CA 2,312,109
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: Arg at position 1 is modified at its amino group with a decanoyl
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (4)..(4)
; OTHER INFORMATION: Arg at position 4 is modified at its carboxyl group with a -CH2Cl
US-09-885-914B-3

Query Match 100.0%; Score 19; DB 11; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVKR 4
Db 1 RVKR 4

RESULT 2
US-10-478-179-8
; Sequence 8, Application US/10478179
; Publication No. US20040249126A1
; GENERAL INFORMATION:
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: CHIMERIC ANTIGEN-SPECIFIC T
; FILE OF INVENTION: CELL-ACTIVATING POLYPEPTIDES
; FILE REFERENCE: 07039-277US1
; CURRENT APPLICATION NUMBER: US/10/478,179

; CURRENT FILING DATE: 2003-11-18
; PRIOR APPLICATION NUMBER: PCT/US02/15992
; PRIOR FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 60/291,874
; PRIOR FILING DATE: 2001-05-18
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: linker peptide
US-10-478-179-8

Query Match 100.0%; Score 19; DB 16; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVKR 4
Db 1 RVKR 4

RESULT 3
US-09-977-831-29
; Sequence 29, Application US/09977831
; Patent No. US20020120100A1
; GENERAL INFORMATION:
; APPLICANT: PACTT, Tech Transfer Office University of Lausanne
; APPLICANT: Bonny, Christophe
; TITLE OF INVENTION: INTRACELLULAR DELIVERY OF BIOLOGICAL EFFECTORS
; FILE REFERENCE: 20349-512 Transporter peptides
; CURRENT APPLICATION NUMBER: US/09/977,831
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/240,315
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: TRANSPORTER
; OTHER INFORMATION: PEPTIDE
US-09-977-831-29

Query Match 84.2%; Score 16; DB 9; Length 4;
Best Local Similarity 75.0%; Pred. No. 1.5e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVKR 4
Db 1 RVKR 4

RESULT 4
US-10-165-015-29
; Sequence 29, Application US/10165015
; Publication No. US20030032594A1
; GENERAL INFORMATION:
; APPLICANT: PACTT, Tech Transfer Office University of Lausanne
; APPLICANT: Bonny, Christophe
; TITLE OF INVENTION: INTRACELLULAR DELIVERY OF BIOLOGICAL EFFECTORS
; FILE REFERENCE: 20349-512 CIP
; CURRENT APPLICATION NUMBER: US/10/165,015
; CURRENT FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 09/977,831
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/240,315
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 37

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVKR 4
|:|
Db 1 RLKR 4

RESULT 9

US-09-887-669-12
; Sequence 12, Application US/09887669
; Publication No. US20020082397A1
; GENERAL INFORMATION:
; APPLICANT: SCHLESSINGER, JOSEPH
; APPLICANT: SAP, JAN M.
; APPLICANT: ULLRICH, AXEL
; APPLICANT: VOGEL, WOLFGANG
; APPLICANT: FUCHS, MIRIAM
; TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE PHOSPHATASE-KAPPA
; FILE REFERENCE: 038602/1246
; CURRENT APPLICATION NUMBER: US/09/887,669
; CURRENT FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: 09/234,883
; PRIOR FILING DATE: 1999-01-21
; PRIOR APPLICATION NUMBER: 08/087,244
; PRIOR FILING DATE: 1993-07-01
; PRIOR APPLICATION NUMBER: 08/049,384
; PRIOR FILING DATE: 1993-04-21
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
; OTHER INFORMATION: cleavage motif
US-09-887-669-12

Query Match 78.9%; Score 15; DB 9; Length 4;
Best Local Similarity 75.0%; Pred. No. 1.5e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RVKR 4
|:|
Db 1 RTKR 4

RESULT 10

US-09-841-730-23
; Sequence 23, Application US/09841730
; Patent No. US20020157126A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; APPLICANT: McPherron, Alexandra C.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR RECEPTORS,
; TITLE OF INVENTION: AGONISTS AND ANTAGONISTS THEREOF, AND METHODS OF USING SAME
; FILE REFERENCE: JHU1470-2
; CURRENT APPLICATION NUMBER: US/09/841,730
; CURRENT FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 09/626,896
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 09/485,046
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: PCT/US98/15598
; PRIOR FILING DATE: 1998-07-28
; PRIOR APPLICATION NUMBER: 60/054,461
; PRIOR FILING DATE: 1997-08-01
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Eukaryotes

; FEATURE:
; NAME/KEY: SITE
; LOCATION: (0)...(0)
; OTHER INFORMATION: proteolytic processing site
US-09-841-730-23

Query Match 78.9%; Score 15; DB 9; Length 4;
Best Local Similarity 50.0%; Pred. No. 1.5e+06;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVKR 4
|:|
Db 1 RIRR 4

RESULT 11

US-09-997-868-22
; Sequence 22, Application US/09997868
; Publication No. US20030031654A1
; GENERAL INFORMATION:
; APPLICANT: Gorman, Cornelia M.,
; Groskreutz, Debyra J.
; TITLE OF INVENTION: Prohormone Convertase Transformed Cells and
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/997,868
FILING DATE: 12-Mar-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/887265
FILING DATE: 22-MAY-1992
APPLICATION NUMBER: 07/803631
FILING DATE: 06-DEC-1992
APPLICATION NUMBER: PCT/US92/10621
FILING DATE: 04-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P0748P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-997-868-22

Query Match 78.9%; Score 15; DB 10; Length 4;
Best Local Similarity 75.0%; Pred. No. 1.5e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RVKR 4
|:|
Db 1 RTKR 4

RESULT 12

US-10-013-032-23
; Sequence 23, Application US/10013032
; Publication No. US20020155544A1
; GENERAL INFORMATION:
; APPLICANT: Hullett, Debra A
; APPLICANT: Alam, Tausif
; APPLICANT: Sollinger, Hans W.
; TITLE OF INVENTION: Treatment of Diabetes with Synthetic Beta Cells
; FILE REFERENCE: 96429/9003CIP
; CURRENT APPLICATION NUMBER: US/10/013,032
; CURRENT FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/537,696
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/115,888
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:amino acid
; OTHER INFORMATION: sequence of the B-C junction of mutant human
; OTHER INFORMATION: insulin
US-10-013-032-23

Query Match 78.9%; Score 15; DB 13; Length 4;
Best Local Similarity 75.0%; Pred. No. 1.5e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RVKR 4
Db 1 RTKR 4

RESULT 13
US-10-074-956-26
; Sequence 26, Application US/10074956
; Publication No. US2002019332A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; TITLE OF INVENTION: METHODS OF TREATING BLADDER DISORDERS
; FILE REFERENCE: 08191-022001
; CURRENT APPLICATION NUMBER: US/10/074,956
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 60/268,175
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Furin site
US-10-074-956-26

Query Match 78.9%; Score 15; DB 13; Length 4;
Best Local Similarity 50.0%; Pred. No. 1.5e+06;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVKR 4
Db 1 RTRR 4

RESULT 14
US-10-115-134-60
; Sequence 60, Application US/10115134
; Publication No. US2003022397A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur Charles

; APPLICANT: GUTERMAN, Sonia Kosow
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel Baribault
; APPLICANT: ROBERTS, Bruce Lindsay
; APPLICANT: LADNER, Robert Charles
; TITLE OF INVENTION: DOMAIN MUTANTS AS CATHEPSIN G INHIBITORS
; FILE REFERENCE: LEY-1C
; CURRENT APPLICATION NUMBER: US/10/115,134
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 08/849,406
; PRIOR FILING DATE: 2001-07-21
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 60
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: 39-42 of BRINK
US-10-115-134-60

Query Match 78.9%; Score 15; DB 15; Length 4;
Best Local Similarity 75.0%; Pred. No. 1.5e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RVKR 4
Db 1 RAKR 4

RESULT 15
US-10-831-302-15
; Sequence 15, Application US/10831302
; Publication No. US20050003482A1
; GENERAL INFORMATION:
; APPLICANT: Fang, Jianmin
; APPLICANT: Jooss, Karin
; APPLICANT: Qian, Jing-Jing
; TITLE OF INVENTION: Compositions and Methods for Enhanced Expression of
; TITLE OF INVENTION: Immunoglobulins From A Single Vector Using a Peptide
; TITLE OF INVENTION: Cleavage Site
; FILE REFERENCE: 3802-092-27CIP
; CURRENT APPLICATION NUMBER: US/10/831,302
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: US 10/452,253
; PRIOR FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: US 60/540,554
; PRIOR FILING DATE: 2004-02-02
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: furin cleavage site sequence
US-10-831-302-15

Query Match 78.9%; Score 15; DB 17; Length 4;
Best Local Similarity 75.0%; Pred. No. 1.5e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RVKR 4
Db 1 RAKR 4

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Job time : 106 secs

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OM protein - protein search, using sw model

Run on: June 20, 2005, 16:24:07 ; Search time 328.5 Seconds
(without alignments)
14.222 Million cell updates/sec

Title: US-09-885-914B-3

Perfect score: 19

Sequence: 1 RVKR 4

Scoring table: BLOSUM62

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Searched: 6959266 seqs, 116806243 residues

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Minimum DB seq length: 0

Maximum DB seq length: 4

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Pending Patents AA Main:*

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2: /cgn2_6/ptodata/1/paa/US06 COMB.pep.*
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6: /cgn2_6/ptodata/1/paa/US082 COMB.pep.*
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37: /cgn2_6/ptodata/1/paa/US60 COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	19	100.0	4	23	US-09-885-914B-3	Sequence 3, Appli
2	19	100.0	4	30	US-10-478-179-8	Sequence 8, Appli
3	16	84.2	4	1	PCT-US02-19394-69	Sequence 69, Appl
4	16	84.2	4	1	PCT-US03-05015-19	Sequence 19, Appl
5	16	84.2	4	7	US-08-398-028A-73	Sequence 73, Appl
6	16	84.2	4	8	US-08-460-343A-73	Sequence 73, Appl
7	16	84.2	4	9	US-08-504-265A-73	Sequence 73, Appl
8	16	84.2	4	17	US-09-372-003-4	Sequence 4, Appli
9	16	84.2	4	17	US-09-372-003-20	Sequence 20, Appl
10	16	84.2	4	19	US-09-566-922A-19	Sequence 19, Appl
11	16	84.2	4	19	US-09-566-922C-19	Sequence 19, Appl
12	16	84.2	4	25	US-09-977-831-29	Sequence 29, Appl
13	16	84.2	4	27	US-10-155-886-24	Sequence 24, Appl
14	16	84.2	4	27	US-10-165-015-29	Sequence 29, Appl
15	16	84.2	4	27	US-10-173-524-69	Sequence 69, Appl
16	16	84.2	4	29	US-10-393-127-29	Sequence 29, Appl
17	16	84.2	4	30	US-10-428-868-33	Sequence 33, Appl
18	16	84.2	4	32	US-10-641-834-3	Sequence 3, Appli
19	16	84.2	4	37	US-60-360-967-19	Sequence 19, Appl
20	15	78.9	4	1	PCT-US01-23510-23	Sequence 23, Appl
21	15	78.9	4	1	PCT-US02-19394-68	Sequence 68, Appl
22	15	78.9	4	1	PCT-US04-12793-38	Sequence 38, Appl
23	15	78.9	4	1	PCT-US04-12807-15	Sequence 15, Appl
24	15	78.9	4	3	US-07-887-265A-22	Sequence 22, Appl
25	15	78.9	4	6	US-08-200-900-36	Sequence 36, Appl
26	15	78.9	4	6	US-08-200-900-38	Sequence 38, Appl
27	15	78.9	4	6	US-08-244-121-22	Sequence 22, Appl
28	15	78.9	4	6	US-08-271-943-16	Sequence 16, Appl
29	15	78.9	4	9	US-08-504-265A-86	Sequence 86, Appl
30	15	78.9	4	14	US-09-011-006C-49	Sequence 49, Appl
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32	15	78.9	4	19	US-09-517-906B-15	Sequence 15, Appl
33	15	78.9	4	20	US-09-628-112-23	Sequence 23, Appl
34	15	78.9	4	21	US-09-708-693-23	Sequence 23, Appl
35	15	78.9	4	23	US-09-841-730-23	Sequence 23, Appl
36	15	78.9	4	24	US-09-887-669-12	Sequence 12, Appl
37	15	78.9	4	24	US-09-906-206A-58	Sequence 58, Appl
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39	15	78.9	4	25	US-09-997-868-22	Sequence 22, Appl
40	15	78.9	4	26	US-10-013-032-23	Sequence 23, Appl
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42	15	78.9	4	27	US-10-115-134-60	Sequence 60, Appl
43	15	78.9	4	27	US-10-173-524-68	Sequence 68, Appl
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45	15	78.9	4	34	US-10-831-304-38	Sequence 38, Appl
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47	15	78.9	4	36	US-11-019-955-26	Sequence 26, Appl
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49	14	73.7	4	1	PCT-US04-00901-49	Sequence 49, Appl
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53	14	73.7	4	11	US-08-716-345A-7	Sequence 7, Appli
54	14	73.7	4	12	US-08-814-394A-33	Sequence 33, Appl
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62	14	73.7	4	23	US-09-813-653-11	Sequence 11, Appl
63	14	73.7	4	26	US-10-045-612A-23	Sequence 23, Appl
64	14	73.7	4	26	US-10-057-620-17	Sequence 17, Appl
65	14	73.7	4	28	US-10-215-272-34	Sequence 34, Appl
66	14	73.7	4	29	US-10-328-813-11	Sequence 11, Appl
67	14	73.7	4	30	US-10-428-868-7	Sequence 7, Appli
68	14	73.7	4	32	US-10-641-834-5	Sequence 5, Appli
69	14	73.7	4	33	US-10-715-976-34	Sequence 34, Appl

70 14 73.7 4 33 US-10-716-326-34 Sequence 34, Appl
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72 13 68.4 4 1 PCT-US02-02814-43 Sequence 43, Appl
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83 13 68.4 4 1 PCT-US04-23191-20 Sequence 20, Appl
84 13 68.4 4 1 PCT-US04-23192-20 Sequence 20, Appl
85 13 68.4 4 1 PCT-US97-01470-39 Sequence 39, Appl
86 13 68.4 4 1 PCT-US98-25372-6 Sequence 6, Appl
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93 13 68.4 4 7 US-08-385-209-20 Sequence 20, Appl
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95 13 68.4 4 14 US-09-006-298-28 Sequence 28, Appl
96 13 68.4 4 14 US-09-011-006C-52 Sequence 52, Appl
97 13 68.4 4 14 US-09-049-770-4 Sequence 4, Appl
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99 13 68.4 4 14 US-09-054-801A-1 Sequence 1, Appl
100 13 68.4 4 16 US-09-287-145-56 Sequence 56, Appl

ALIGNMENTS

RESULT 1
US-09-885-914B-3
; Sequence 3, Application US/09885914B
; GENERAL INFORMATION:
; APPLICANT: DUBOIS, Claire
; TITLE OF INVENTION: USE OF FURIN AND FURIN-LIKE PROTEASE INHIBITORS IN THE TREATMENT
; FILE REFERENCE: 85761-28
; CURRENT APPLICATION NUMBER: US/09/885, 914B
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/213, 995
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: CA 2,312,109
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: Arg at position 1 is modified at its amino group with a decanoyl
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (4)..(4)
; OTHER INFORMATION: Arg at position 4 is modified at its carboxyl group with a -CH2CH3
US-09-885-914B-3
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Best Local Similarity 100.0%; Pred. No. 6.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RVKR 4

Db 1 RVKR 4
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US-10-478-179-8
; Sequence 8, Application US/10478179
; GENERAL INFORMATION:
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: CHIMERIC ANTIGEN-SPECIFIC T
; FILE REFERENCE: 07039-277US1
; CURRENT APPLICATION NUMBER: US/10/478,179
; CURRENT FILING DATE: 2003-11-18
; PRIOR APPLICATION NUMBER: PCT/US02/15992
; PRIOR FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 60/291,874
; PRIOR FILING DATE: 2001-05-18
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: linker peptide
US-10-478-179-8
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Best Local Similarity 100.0%; Pred. No. 6.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RVKR 4
Db 1 RVKR 4
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PCT-US02-19394-69
; Sequence 69, Application PC/TUS0219394
; GENERAL INFORMATION:
; APPLICANT: Komiya, Tomoko
; APPLICANT: Fuller, Robert S.
; TITLE OF INVENTION: Eglin C Based Drugs for Treatment of Disease
; FILE REFERENCE: UM-07240
; CURRENT APPLICATION NUMBER: PCT/US02/19394
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: 60/299,096
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69
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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
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Best Local Similarity 75.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 RVKR 4
Db 1 RVKR 4
RESULT 4
PCT-US03-05015-19
; Sequence 19, Application PC/TUS0305015
; GENERAL INFORMATION:
; APPLICANT: Board of Regents of the University of Nebraska

APPLICANT: Sanderson, Sam D.G.
APPLICANT: Vennerstrom, Jonathan L.
APPLICANT: Thiele, Geoffrey M.
APPLICANT: Parameswaran, Maniyan
APPLICANT: Bevins, Rick A.
APPLICANT: Srinivasa, Cheruku R.
TITLE OF INVENTION: Compositions and compounds for use as a
TITLE OF INVENTION: nicotine vaccine employing response selective agonist of an
TITLE OF INVENTION: antigen-presenting cell receptor as a molecular adjuvant
FILE REFERENCE: UNMCS744.1
CURRENT APPLICATION NUMBER: PCT/US03/05015
PRIOR FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/360,967
PRIOR FILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 19
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Sequence
PCT-US03-05015-19

Query Match 84.2%; Score 16; DB 1; Length 4;
Best Local Similarity 75.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVKR 4
||:|
Db 1 RVR 4

RESULT 5

US-08-398-028A-73
Sequence 73, Application US/08398028A
GENERAL INFORMATION:
APPLICANT: Marcus D. Ballinger and James A. Wells
TITLE OF INVENTION: SUBSTITIN VARIANTS CAPABLE OF CLEAVING
TITLE OF INVENTION: SUBSTRATES CONTAINING DIBASIC RESIDUES
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/398,028A
FILING DATE: 03-Mar-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kubinec, Jeffrey S.
REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: P0936
TELEPHONE: 415/225-8228
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

US-08-398-028A-73
Query Match 84.2%; Score 16; DB 7; Length 4;
Best Local Similarity 75.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVKR 4
||:|
Db 1 RVR 4

Best Local Similarity 75.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVKR 4
||:|
Db 1 RVR 4

RESULT 6

US-08-460-343A-73
Sequence 73, Application US/08460343A
GENERAL INFORMATION:
APPLICANT: Marcus D. Ballinger and James A. Wells
TITLE OF INVENTION: SUBSTITIN VARIANTS CAPABLE OF CLEAVING
TITLE OF INVENTION: SUBSTRATES CONTAINING DIBASIC RESIDUES
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,343A
FILING DATE: 01-Jun-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/398028
FILING DATE: 03-mar-1995
ATTORNEY/AGENT INFORMATION:
NAME: Kubinec, Jeffrey S.
REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: P0936C1
TELEPHONE: 415/225-8228
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-460-343A-73

Query Match 84.2%; Score 16; DB 8; Length 4;
Best Local Similarity 75.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVKR 4
||:|
Db 1 RVR 4

RESULT 7

US-08-504-265A-73
Sequence 73, Application US/08504265A
GENERAL INFORMATION:
APPLICANT: Marcus D. Ballinger and James A. Wells
TITLE OF INVENTION: SUBSTITIN VARIANTS CAPABLE OF
TITLE OF INVENTION: CLEAVING SUBSTRATES CONTAINING BASIC RESIDUES
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA

US-08-504-265A-73
Query Match 84.2%; Score 16; DB 8; Length 4;
Best Local Similarity 75.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVKR 4
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Db 1 RVR 4

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; COMPUTER: IBM PC compatible
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; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/504,265A
; FILING DATE: 19-Jul-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/398028
; FILING DATE: 03-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Kubinec, Jeffrey S.
; REGISTRATION NUMBER: 36,575
; REFERENCE/DOCKET NUMBER: P0936P1
; TELEPHONE: 415/225-8228
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
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; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-504-265A-73
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; Query Match 84.2%; Score 16; DB 9; Length 4;
; Best Local Similarity 75.0%; Pred. No. 6.4e+06;
; Mismatches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 1 RVKR 4
Db ||:|
1 RVRR 4
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; RESULT 8
; US-09-372-003-4
; Sequence 4, Application US/09372003
; GENERAL INFORMATION:
; APPLICANT: Thomas, Gary
; APPLICANT: Anderson, Eric D
; APPLICANT: Thomas, Laurel
; APPLICANT: Hayflick, Joel S
; APPLICANT: Nelson, Jay
; APPLICANT: Stenglen, Stephan G
; TITLE OF INVENTION: Methods and Reagents for Inhibiting Furin
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/372,003
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/481,534
; FILING DATE: 14-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Noonan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,448-D
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; TELEX:
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified site
; LOCATION: 1..4
; OTHER INFORMATION: /label=Modified site
; OTHER INFORMATION: / note="The amino terminus us derivatized by a
; OTHER INFORMATION: butoxycarbonyl group, and the carboxyl terminus
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-372-003-4
;
; Query Match 84.2%; Score 16; DB 17; Length 4;
; Best Local Similarity 75.0%; Pred. No. 6.4e+06;
; Mismatches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 1 RVKR 4
Db ||:|
1 RVRR 4
;
; RESULT 9
; US-09-372-003-20
; Sequence 20, Application US/09372003
; GENERAL INFORMATION:
; APPLICANT: Thomas, Gary
; APPLICANT: Anderson, Eric D
; APPLICANT: Thomas, Laurel
; APPLICANT: Hayflick, Joel S
; APPLICANT: Nelson, Jay
; APPLICANT: Stenglen, Stephan G
; TITLE OF INVENTION: Methods and Reagents for Inhibiting Furin
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/372,003
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/481,534
; FILING DATE: 14-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Noonan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,448-D
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
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; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
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; NAME/KEY: Modified site
; LOCATION: 1..4
; OTHER INFORMATION: /label=Modified site
; OTHER INFORMATION: / note="The amino terminus us derivatized by a
; OTHER INFORMATION: butoxycarbonyl group, and the carboxyl terminus
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OTHER INFORMATION: is derivatized by a 4-methylcoumaryl-7-amide group."
US-09-372-003-20

Query Match 84.2%; Score 16; DB 17; Length 4;
Best Local Similarity 75.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVRK 4
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Db 1 RVRK 4

RESULT 10

US-09-566-922A-19
; Sequence 19, Application US/09566922A
; GENERAL INFORMATION:
; APPLICANT: The Board of Regents of the University of Nebraska
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ENHANCING IMMUNE RESPONSES MEDIATED
; FILE REFERENCE: UNMC5736
; CURRENT APPLICATION NUMBER: US/09/566,922A
; CURRENT FILING DATE: 2000-05-05
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: PCT/US96/16825
; PRIOR FILING DATE: 1996-10-18
; PRIOR APPLICATION NUMBER: US 60/005,727
; PRIOR FILING DATE: 1995-10-20
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: synthetic sequence
US-09-566-922A-19

Query Match 84.2%; Score 16; DB 19; Length 4;
Best Local Similarity 75.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVRK 4
||:|
Db 1 RVRK 4

RESULT 11

US-09-566-922C-19
; Sequence 19, Application US/09566922C
; GENERAL INFORMATION:
; APPLICANT: The Board of Regents of the University of Nebraska
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ENHANCING IMMUNE RESPONSES MEDIATED
; FILE REFERENCE: UNMC5736
; CURRENT APPLICATION NUMBER: US/09/566,922C
; CURRENT FILING DATE: 2000-05-05
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: PCT/US96/16825
; PRIOR FILING DATE: 1996-10-18
; PRIOR APPLICATION NUMBER: US 60/005,727
; PRIOR FILING DATE: 1995-10-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic sequence

US-09-566-922C-19

Query Match 84.2%; Score 16; DB 19; Length 4;
Best Local Similarity 75.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVRK 4
||:|
Db 1 RVRK 4

RESULT 12

US-09-977-831-29
; Sequence 29, Application US/09977831
; GENERAL INFORMATION:
; APPLICANT: PACTT, Tech Transfer Office University of Lausanne
; APPLICANT: Bonny, Christophe
; TITLE OF INVENTION: INTRACELLULAR DELIVERY OF BIOLOGICAL EFFECTORS
; FILE REFERENCE: 20349-512 Transporter peptides
; CURRENT APPLICATION NUMBER: US/09/977,831
; CURRENT FILING DATE: 2001-10-15
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: TRANSPORTER
; OTHER INFORMATION: PEPTIDE
US-09-977-831-29

Query Match 84.2%; Score 16; DB 25; Length 4;
Best Local Similarity 75.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVRK 4
||:|
Db 1 RVRK 4

RESULT 13

US-10-155-886-24
; Sequence 24, Application US/10155886
; GENERAL INFORMATION:
; APPLICANT: Hempstead, Barbara L.
; APPLICANT: Lee, Ramee
; APPLICANT: Teng, Kenneth K.
; APPLICANT: Kermani, Pouneh
; TITLE OF INVENTION: High Affinity Ligand For p75 Neurotrophin Receptor
; FILE REFERENCE: 955-21 Sequence Nos. 1-68
; CURRENT APPLICATION NUMBER: US/10/155,886
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-155-886-24

Query Match 84.2%; Score 16; DB 27; Length 4;
Best Local Similarity 75.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVRK 4
||:|
Db 1 RVRK 4

RESULT 14

US-10-165-015-29
; Sequence 29, Application US/10165015
; GENERAL INFORMATION:
; APPLICANT: PACTI, Tech Transfer Office University of Lausanne
; APPLICANT: Bonny, Christophe
; TITLE OF INVENTION: INTRACELLULAR DELIVERY OF BIOLOGICAL EFFECTORS
; FILE REFERENCE: 20349-512 CIP
; CURRENT APPLICATION NUMBER: US/10/165,015
; CURRENT FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 09/977,831
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/240,315
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: TRANSPORTER
; OTHER INFORMATION: PEPTIDE
US-10-165-015-29

Query Match 84.2%; Score 16; DB 27; Length 4;
Best Local Similarity 75.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVKR 4
|||
Db 1 RVRK 4

RESULT 15
US-10-173-524-69
; Sequence 69, Application US/10173524
; GENERAL INFORMATION:
; APPLICANT: Komiyama, Tomoko
; APPLICANT: Fuller, Robert S.
; TITLE OF INVENTION: Eglin C Based Drugs for Treatment of Disease
; FILE REFERENCE: UM-07240
; CURRENT APPLICATION NUMBER: US/10/173,524
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: 60/299,096
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-173-524-69

Query Match 84.2%; Score 16; DB 27; Length 4;
Best Local Similarity 75.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVKR 4
|||
Db 1 RVRK 4

Search completed: June 20, 2005, 16:46:44
Job time : 330.5 secs

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OM protein - protein search, using sw model

Run on: June 20, 2005, 16:30:17 ; Search time 37 Seconds
(without alignments)
13.327 Million cell updates/sec

Title: US-09-885-914B-3

Perfect score: 19

Sequence: 1 RVKR 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 583429 seqs, 123271311 residues

Total number of hits satisfying chosen parameters: 4687

Minimum DB seq length: 0

Maximum DB seq length: 4

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Pending Patents AA New:
1: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep.*
2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep.*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep.*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep.*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep.*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep.*
7: /cgn2_6/ptodata/2/paa/US11_NEW_COMB.pep.*
8: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16	84.2	4	6	US-10-892-402-110
2	15	78.9	4	5	US-09-997-868A-22
3	15	78.9	4	6	US-10-857-498A-11
4	15	78.9	4	7	US-11-051-267-23
5	15	78.9	4	7	US-11-127-629-23
6	14	73.7	4	7	US-11-129-741-2596
7	13	68.4	4	5	US-09-997-868A-23
8	13	68.4	4	6	US-10-892-402-107
9	13	68.4	4	6	US-10-892-402-108
10	13	68.4	4	6	US-10-892-402-109
11	13	68.4	4	6	US-10-386-414A-25
12	13	68.4	4	6	US-10-061-395B-43
13	13	68.4	4	7	US-11-004-794A-81
14	13	68.4	4	7	US-11-004-795A-97
15	13	68.4	4	7	US-11-107-481-17
16	13	68.4	4	7	US-11-004-399-1871
17	13	68.4	4	7	US-11-126-817-55
18	13	68.4	4	7	US-11-127-629-19
19	12	63.2	4	5	US-09-997-868A-24
20	12	63.2	4	6	US-10-892-402-122
21	12	63.2	4	7	US-11-065-669-23
22	12	63.2	4	7	US-11-080-973-23
23	12	63.2	4	7	US-11-106-718-21
24	12	63.2	4	7	US-11-129-741-2008
25	11	57.9	4	5	US-09-978-498-12

26	11	57.9	4	5	US-09-784-950A-106
27	11	57.9	4	6	US-10-356-656-13
28	11	57.9	4	6	US-10-892-402-12
29	11	57.9	4	6	US-10-892-402-60
30	11	57.9	4	6	US-10-892-402-102
31	11	57.9	4	6	US-10-892-402-106
32	11	57.9	4	6	US-10-892-402-146
33	11	57.9	4	6	US-10-892-402-152
34	11	57.9	4	6	US-10-684-796-380
35	11	57.9	4	6	US-10-071-395-12
36	11	57.9	4	7	US-11-004-399-3559
37	11	57.9	4	7	US-11-033-039-3
38	11	57.9	4	7	US-11-033-039-8
39	11	57.9	4	7	US-11-033-039-801
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43	10	52.6	3	1	PCT-US04-26288-120
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51	10	52.6	3	1	PCT-US04-26288-165
52	10	52.6	3	1	PCT-US04-26288-169
53	10	52.6	3	1	PCT-US05-11740-7
54	10	52.6	3	6	US-10-472-963-801
55	10	52.6	3	6	US-10-994-612-15
56	10	52.6	3	6	US-10-994-612-19
57	10	52.6	4	1	PCT-US05-04041-44
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60	10	52.6	4	1	PCT-US04-26288-238
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62	10	52.6	4	1	PCT-US04-26288-238
63	10	52.6	4	1	PCT-US04-26288-239
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67	10	52.6	4	1	PCT-US04-26288-292
68	10	52.6	4	1	PCT-US04-26288-293
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70	10	52.6	4	1	PCT-US04-26288-299
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78	10	52.6	4	1	PCT-US04-26288-317
79	10	52.6	4	1	PCT-US04-26288-384
80	10	52.6	4	1	PCT-US04-26288-386
81	10	52.6	4	1	PCT-US04-26288-401
82	10	52.6	4	1	PCT-US04-26288-409
83	10	52.6	4	1	PCT-US04-26288-411
84	10	52.6	4	1	PCT-US04-26288-414
85	10	52.6	4	1	PCT-US04-26288-415
86	10	52.6	4	1	PCT-US04-26288-416
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89	10	52.6	4	1	PCT-US04-26288-420
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93	10	52.6	4	1	PCT-US04-26288-425
94	10	52.6	4	1	PCT-US04-26288-426
95	10	52.6	4	1	PCT-US04-26288-427
96	10	52.6	4	1	PCT-US04-26288-428
97	10	52.6	4	1	PCT-US04-26288-430
98	10	52.6	4	1	PCT-US04-26288-431

Sequence 106, App
Sequence 13, Appl
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Sequence 102, App
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Sequence 146, App
Sequence 152, App
Sequence 380, App
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Sequence 8, Appli
Sequence 801, App
Sequence 109, App
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Sequence 119, App
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Sequence 427, App
Sequence 428, App
Sequence 430, App
Sequence 431, App

Sequence 432, App
Sequence 449, App

99 10 52.6 4 1 PCT-US04-26288-432
100 10 52.6 4 1 PCT-US04-26288-449

ALIGNMENTS

RESULT 1
US-10-892-402-110
; Sequence 110, Application US/10892402
; GENERAL INFORMATION:
; APPLICANT: Harris, Jennifer L.
; APPLICANT: Damoiseaux, Robert
; APPLICANT: Backes, Bradley J.
; APPLICANT: Winesinger, Nicolas
; APPLICANT: TRM LLC
; TITLE OF INVENTION: Fluorogenic Enzyme Substrates and Uses
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 021288-000410US
; CURRENT APPLICATION NUMBER: US/10/892,402
; CURRENT FILING DATE: 2004-07-14
; PRIOR APPLICATION NUMBER: US 60/487,464
; PRIOR FILING DATE: 2003-07-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 110
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: rhodamine protease substrate library peptide
US-10-892-402-110

Query Match 84.2%; Score 16; DB 6; Length 4;
Best Local Similarity 75.0%; Pred. No. 5.4e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVKR 4
Db 1 RVRR 4

RESULT 2
US-09-997-868A-22
; Sequence 22, Application US/09997868A
; GENERAL INFORMATION:
; APPLICANT: Gorman, Cornelia M.
; APPLICANT: Groskreutz, Debyra J.
; TITLE OF INVENTION: PROHORMONE CONVERTASE TRANSFORMED CELLS AND POLYPEPTIDE SYNTHESIS
; FILE REFERENCE: 11669.103USW3
; CURRENT APPLICATION NUMBER: US/09/997,868A
; CURRENT FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 08/026,143
; PRIOR FILING DATE: 1993-03-01
; PRIOR APPLICATION NUMBER: PCT/US92/10621
; PRIOR FILING DATE: 1992-12-04
; PRIOR APPLICATION NUMBER: US 07/887,265
; PRIOR FILING DATE: 1992-05-22
; PRIOR APPLICATION NUMBER: US 07/803,631
; PRIOR FILING DATE: 1991-12-06
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Peptide
US-09-997-868A-22

Query Match 78.9%; Score 15; DB 5; Length 4;
Best Local Similarity 75.0%; Pred. No. 5.4e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RVKR 4
Db 1 RTKR 4

RESULT 3
US-10-857-498A-11
; Sequence 11, Application US/10857498A
; GENERAL INFORMATION:
; APPLICANT: Ko, Derek
; APPLICANT: Li, Yuanhao
; APPLICANT: Harding, Thomas
; APPLICANT: Fang, Jianmin
; APPLICANT: Ramesh, Nagarajan
; APPLICANT: Yu, De Chao
; TITLE OF INVENTION: Cell Specific Replication-Competent Viral Vectors Comprising
; TITLE OF INVENTION: a Self Processing Peptide Cleavage Site
; FILE REFERENCE: 3802-095-27
; CURRENT APPLICATION NUMBER: US/10/857,498A
; CURRENT FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/475,005
; PRIOR FILING DATE: 2003-06-03
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: exemplary additional proteolytic cleavage site
US-10-857-498A-11

Query Match 78.9%; Score 15; DB 6; Length 4;
Best Local Similarity 75.0%; Pred. No. 5.4e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RVKR 4
Db 1 RAKR 4

RESULT 4
US-11-051-267-23
; Sequence 23, Application US/11051267
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; APPLICANT: McPherron, Alexandra C.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR RECEPTORS,
; TITLE OF INVENTION: AGONISTS AND ANTAGONISTS THEREOF, AND METHODS OF USING SAME
; FILE REFERENCE: JHUI470-2
; CURRENT APPLICATION NUMBER: US/11/051,267
; CURRENT FILING DATE: 2005-02-03
; PRIOR APPLICATION NUMBER: US/09/841,730
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 09/626,896
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 09/485,046
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: PCT/US98/15598
; PRIOR FILING DATE: 1998-07-28
; PRIOR APPLICATION NUMBER: 60/054,461
; PRIOR FILING DATE: 1997-08-01
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Eukaryotes
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (0)...(0)
; OTHER INFORMATION: proteolytic processing site

US-11-051-267-23

Query Match 78.9%; Score 15; DB 7; Length 4;
Best Local Similarity 50.0%; Pred. No. 5.4e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVKR 4
|:|
Db 1 RIRR 4

RESULT 5

US-11-127-629-23
; Sequence 23, Application US/11127629
; GENERAL INFORMATION:
; APPLICANT: Alam, Tausif
; APPLICANT: Hullett, Debra A.
; APPLICANT: Sollinger, Hans W.
; TITLE OF INVENTION: Treatment of Diabetes with Synthetic Beta Cells
; FILE REFERENCE: 960296.00216
; CURRENT APPLICATION NUMBER: US/11/127,629
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 10/923,924
; PRIOR FILING DATE: 2004-08-23
; PRIOR APPLICATION NUMBER: 10/013,032
; PRIOR FILING DATE: 2001-11-12
; PRIOR APPLICATION NUMBER: 09/537,696
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 09/115,888
; PRIOR FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: 08/786,625
; PRIOR FILING DATE: 1997-01-21
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 23
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: amino acid sequence of the B-C junction of mutant human insulin
US-11-127-629-23

Query Match 78.9%; Score 15; DB 7; Length 4;
Best Local Similarity 75.0%; Pred. No. 5.4e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RVKR 4
|:|
Db 1 RTKR 4

RESULT 6

US-11-129-741-2596
; Sequence 2596, Application US/11129741
; GENERAL INFORMATION:
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: WOO, CHIU YAT PATRICK
; APPLICANT: LAU, KAR PUI SUSANNA
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: PEIRIS, JOSEPH S.M.
; APPLICANT: GUAN, YI
; TITLE OF INVENTION: A NOVEL HUMAN VIRUS CAUSING RESPIRATORY TRACT
; TITLE OF INVENTION: INFECTION AND USES THEREOF
; FILE REFERENCE: V0690, 0044
; CURRENT APPLICATION NUMBER: US/11/129,741
; CURRENT FILING DATE: 2005-05-16
; PRIOR APPLICATION NUMBER: 10/895,064
; PRIOR FILING DATE: 2004-07-21
; NUMBER OF SEQ ID NOS: 4257
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 2596
; LENGTH: 4

; TYPE: PRT
; ORGANISM: Corononavirius-HKU1
US-11-129-741-2596

Query Match 73.7%; Score 14; DB 7; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.4e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVK 3
|:|
Db 2 RVK 4

RESULT 7

US-09-997-868A-23
; Sequence 23, Application US/09997868A
; GENERAL INFORMATION:
; APPLICANT: Gorman, Cornelia M.
; APPLICANT: Groskreutz, Debyra J.
; TITLE OF INVENTION: PROHORMONE CONVERTASE TRANSFORMED CELLS AND POLYPEPTIDE SYNTHESIS
; FILE REFERENCE: 11669.103USW3
; CURRENT APPLICATION NUMBER: US/09/997,868A
; CURRENT FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 08/026,143
; PRIOR FILING DATE: 1993-03-01
; PRIOR APPLICATION NUMBER: PCT/US92/10621
; PRIOR FILING DATE: 1992-12-04
; PRIOR APPLICATION NUMBER: US 07/887,265
; PRIOR FILING DATE: 1992-05-22
; PRIOR APPLICATION NUMBER: US 07/803,631
; PRIOR FILING DATE: 1991-12-06
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 23
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Peptide
US-09-997-868A-23

Query Match 68.4%; Score 13; DB 5; Length 4;
Best Local Similarity 75.0%; Pred. No. 5.4e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RVKR 4
|:|
Db 1 RQKR 4

RESULT 8

US-10-892-402-107
; Sequence 107, Application US/10892402
; GENERAL INFORMATION:
; APPLICANT: Harris, Jennifer L.
; APPLICANT: Damoiseaux, Robert
; APPLICANT: Backes, Bradley J.
; APPLICANT: Winsinger, Nicolas
; APPLICANT: IRM LLC
; TITLE OF INVENTION: Fluorogenic Enzyme Substrates and Uses
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 021288-000410US
; CURRENT APPLICATION NUMBER: US/10/892,402
; CURRENT FILING DATE: 2004-07-14
; PRIOR APPLICATION NUMBER: US 60/487,464
; PRIOR FILING DATE: 2003-07-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: rhodamine protease substrate library peptide
US-10-892-402-107

Query Match 68.4%; Score 13; DB 6; Length 4;
Best Local Similarity 75.0%; Pred. No. 5.4e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RVKR 4
|||
Db 1 RVTR 4

RESULT 9

US-10-892-402-108
; Sequence 108, Application US/10892402
; GENERAL INFORMATION:
; APPLICANT: Harris, Jennifer L.
; APPLICANT: Damoiseaux, Robert
; APPLICANT: Backes, Bradley J.
; APPLICANT: Winssinger, Nicolas
; APPLICANT: IRM LLC
; TITLE OF INVENTION: Fluorogenic Enzyme Substrates and Uses
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 021288-000410US
; CURRENT APPLICATION NUMBER: US/10/892,402
; CURRENT FILING DATE: 2004-07-14
; PRIOR APPLICATION NUMBER: US 60/487,464
; PRIOR FILING DATE: 2003-07-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 108
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: rhodamine protease substrate library peptide
US-10-892-402-108

Query Match 68.4%; Score 13; DB 6; Length 4;
Best Local Similarity 75.0%; Pred. No. 5.4e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RVKR 4
|||
Db 1 RVTR 4

RESULT 10

US-10-892-402-109
; Sequence 109, Application US/10892402
; GENERAL INFORMATION:
; APPLICANT: Harris, Jennifer L.
; APPLICANT: Damoiseaux, Robert
; APPLICANT: Backes, Bradley J.
; APPLICANT: Winssinger, Nicolas
; APPLICANT: IRM LLC
; TITLE OF INVENTION: Fluorogenic Enzyme Substrates and Uses
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 021288-000410US
; CURRENT APPLICATION NUMBER: US/10/892,402
; CURRENT FILING DATE: 2004-07-14
; PRIOR APPLICATION NUMBER: US 60/487,464
; PRIOR FILING DATE: 2003-07-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 109
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: rhodamine protease substrate library peptide
US-10-892-402-109

Query Match 68.4%; Score 13; DB 6; Length 4;
Best Local Similarity 75.0%; Pred. No. 5.4e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RVKR 4
|||
Db 1 RVDR 4

RESULT 11

US-10-386-414A-25
; Sequence 25, Application US/10386414A
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Robison, Keith E.
; APPLICANT: White, David
; APPLICANT: Williamson, Mark W.
; APPLICANT: Cook, William James
; APPLICANT: Meyers, Rachel E.
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Chun, Miyoung
; TITLE OF INVENTION: NOVEL 27875, 22025, 27420, 17906, 16319,
; TITLE OF INVENTION: 55092 AND 10218 MOLECULES AND USES THEREFOR
; FILE REFERENCE: MPI03-0210NMIM
; CURRENT APPLICATION NUMBER: US/10/386,414A
; CURRENT FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: 09/426,282
; PRIOR FILING DATE: 1999-10-25
; PRIOR APPLICATION NUMBER: 09/668,266
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 09/330,970
; PRIOR FILING DATE: 1999-06-11
; PRIOR APPLICATION NUMBER: 09/724,599
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/860,193
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/571,689
; PRIOR FILING DATE: 2000-05-16
; PRIOR APPLICATION NUMBER: 10/283,023
; PRIOR FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: 60/335,044
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 10/010,943
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 60/254,037
; PRIOR FILING DATE: 2000-12-07
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cleavage Site
US-10-386-414A-25

Query Match 68.4%; Score 13; DB 6; Length 4;
Best Local Similarity 75.0%; Pred. No. 5.4e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RVKR 4
|||
Db 1 RKKR 4

RESULT 12

US-10-061-395B-43
; Sequence 43, Application US/10061395B
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice

; APPLICANT: Smith, Ernest S.
; TITLE OF INVENTION: Methods of Identifying Regulator Molecules
; FILE REFERENCE: 1821.0080003
; CURRENT APPLICATION NUMBER: US/10/061,395B
; CURRENT FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 60/271,423
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/265,880
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/265,589
; PRIOR FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heterologous signal sequence for the nucleus
US-10-061-395B-43

Query Match 68.4%; Score 13; DB 6; Length 4;
Best Local Similarity 75.0%; Pred. No. 5.4e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RVKR 4
| | |
Db 1 RKKR 4

RESULT 13

US-11-004-794A-81
; Sequence 81, Application US/11004794A
; GENERAL INFORMATION:
; APPLICANT: Michael Kinch
; TITLE OF INVENTION: Targeted Drug Delivery Using EphA2 or
; FILE REFERENCE: 10271-120-999
; CURRENT APPLICATION NUMBER: US/11/004,794A
; CURRENT FILING DATE: 2004-12-03
; PRIOR APPLICATION NUMBER: 60/527,396
; PRIOR FILING DATE: 2003-12-04
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-004-794A-81

Query Match 68.4%; Score 13; DB 7; Length 4;
Best Local Similarity 75.0%; Pred. No. 5.4e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RVKR 4
| | |
Db 1 RKKR 4

RESULT 14

US-11-004-795A-97
; Sequence 97, Application US/11004795A
; GENERAL INFORMATION:
; APPLICANT: Kinch, Michael
; TITLE OF INVENTION: EphA2, EphA4 and LMW-PTP and Methods of
; FILE REFERENCE: 10271-111-999
; CURRENT APPLICATION NUMBER: US/11/004,795A
; CURRENT FILING DATE: 2004-12-03
; PRIOR APPLICATION NUMBER: 60/527,154
; PRIOR FILING DATE: 2003-12-04
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 97
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-004-795A-97

Query Match 68.4%; Score 13; DB 7; Length 4;
Best Local Similarity 75.0%; Pred. No. 5.4e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RVKR 4
| | |
Db 1 RKKR 4

RESULT 15

US-11-107-481-17
; Sequence 17, Application US/11107481
; GENERAL INFORMATION:
; APPLICANT: Jessell, Thomas M.
; APPLICANT: Basler, Konard
; APPLICANT: Yamada, Toshiya
; TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF DORSALIN-1
; FILE REFERENCE: 0575/40314-A
; CURRENT APPLICATION NUMBER: US/11/107,481
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US/10/002,278
; PRIOR FILING DATE: 2001-11-02
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Chick
US-11-107-481-17

Query Match 68.4%; Score 13; DB 7; Length 4;
Best Local Similarity 75.0%; Pred. No. 5.4e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RVKR 4
| | |
Db 1 RSKR 4

Search completed: June 20, 2005, 16:48:02
Job time : 38 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2005, 19:37:50 ; Search time 41 Seconds
(without alignments)
924.620 Million cell updates/sec

Title: PDX1

Perfect score: 2032

Sequence: 1 EDQGDAAQKTDTSHHDDQH.....IEQNTKSPLEMGKVNPTGK 394

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : PIR 79.*

1: piri.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2003	98.6	418	1 ITHU	alpha-1-antitrypsin
2	1870	92.0	409	1 ITBA	alpha-1-antitrypsin
3	1443.5	71.0	411	1 ITRT	alpha-1-antitrypsin
4	1431.5	70.4	413	2 S60036	alpha-1-antitrypsin
5	1430	70.4	416	1 ITSH	alpha-1-antitrypsin
6	1409	69.3	416	2 S21097	alpha-1-antitrypsin
7	1352	66.5	406	2 JX0346	alpha-1-antitrypsin
8	1335	65.7	413	2 S54981	alpha-1-antitrypsin
9	1327	65.3	413	2 I49470	alpha-1-antitrypsin
10	1322	65.1	413	2 JX0154	alpha-1-antitrypsin
11	1321	65.0	402	2 I49471	alpha-1-antitrypsin
12	1321	65.0	413	2 I49472	alpha-1-antitrypsin
13	1320	65.0	413	2 I49452	alpha-1-antitrypsin
14	1315	64.7	413	2 JX0267	alpha-1-antitrypsin
15	1310	64.5	413	2 I49473	alpha-1-antitrypsin
16	1298	63.9	413	2 A54968	alpha-1-antitrypsin
17	1296	63.8	413	2 I56481	alpha-1-antitrypsin
18	1294	63.7	413	2 I49474	alpha-1-antitrypsin
19	1281.5	63.1	412	1 ITWSC	alpha-1-antitrypsin
20	1280	63.0	405	2 A39088	alpha-1-antitrypsin
21	1235	60.8	410	2 C39088	alpha-1-antitrypsin
22	1181.5	58.1	388	2 B39088	alpha-1-antitrypsin
23	1153.5	55.8	410	2 A45457	alpha-1-antitrypsin
24	1125	55.4	420	2 A28882	alpha-1-antitrypsin
25	834	41.0	410	2 I50494	serine proteinase
26	829	40.8	406	2 A39339	protein C inhibitor
27	824	40.6	418	2 JX0129	contrapsin precursor
28	822	40.5	418	2 S23675	contrapsin-related
29	819	40.3	427	2 A49518	kallistatin precursor

30	816	40.2	433	1 ITHUC	alpha-1-antichymot
31	813.5	40.0	416	2 B29131	kallikrein-binding
32	811.5	39.9	405	2 A28321	corticosteroid-bin
33	806	39.7	406	2 I53281	corticosteroid-bin
34	804	39.6	383	2 A36117	corticosteroid-bin
35	803.5	39.5	418	2 JH0494	alpha-1-antichymot
36	802	39.5	403	2 S08102	serine proteinase
37	797	39.2	408	2 S11320	serine proteinase
38	793	39.0	417	2 S19724	kallikrein-binding
39	788	38.8	430	2 A49190	corticosteroid-bin
40	786.5	38.7	412	2 I46421	thyroxine-binding
41	781.5	38.5	415	2 A47224	thyroxine-binding
42	771.5	38.0	418	1 S31507	serine proteinase
43	771.5	38.0	418	2 A39567	thyroxine-binding
44	750	36.9	412	2 S31505	serine proteinase
45	727	35.8	372	2 I50492	corticosteroid-bin
46	717.5	35.3	397	2 S33415	corticosteroid-bin
47	716.5	35.3	396	2 A40066	corticosteroid-bin
48	708.5	34.9	213	2 A25420	alpha-1-antitrypsin
49	697.5	34.3	369	2 JH0493	alpha-1-antichymot
50	689.5	33.9	436	2 A42440	estrogen-regulated
51	555	27.3	280	2 A29035	thyroid hormone-re
52	546.5	26.9	436	2 JC4841	regeneration assoc
53	529.5	26.1	390	2 I38201	squamous cell carc
54	525.5	25.9	390	2 I38202	leupin precursor -
55	508	25.0	397	2 I39184	bomabin - human
56	507.5	25.0	376	2 B59273	proteinase inhibit
57	505.5	24.9	478	2 A54248	heparin cofactor I
58	498.5	24.5	480	2 I46990	heparin cofactor I
59	498	24.5	252	2 S65289	alpha-1-antichymot
60	495.5	24.4	376	1 A48681	placental thrombin
61	492.5	24.2	479	1 S41066	heparin cofactor I
62	487.5	24.0	378	2 S38962	serpin - pig
63	487.5	24.0	416	2 S19896	plasmaogen activa
64	485	23.9	379	2 A42421	leukocyte elastase
65	482	23.7	415	2 S20047	plasmaogen activa
66	481.5	23.7	378	2 A57488	proteinase inhibit
67	481	23.7	415	2 A32853	plasmaogen activa
68	475.5	23.4	374	2 A59273	proteinase inhibit
69	475.5	23.4	386	1 OACH	ovalbumin (validat
70	468.5	23.1	499	1 A37924	heparin cofactor I
71	468	23.0	400	2 JC4265	plasmaogen activa
72	465	22.9	410	2 S70647	neuroserpin precu
73	459.5	22.6	200	2 D41752	alpha-1-antitrypsin
74	456	22.4	402	1 S06745	plasmaogen activa
75	452	22.2	391	2 JC7118	headpin serine pro
76	446.5	22.0	402	1 ITHUP1	plasmaogen activa
77	440.5	21.7	388	1 DYCH	ovalbumin-related
78	435.5	21.4	465	1 S28219	antithrombin III p
79	432	21.3	420	2 S19208	uteroferin-associ
80	430	21.2	383	2 S11433	ovalbumin - Japane
81	430	21.2	402	1 A35032	plasmaogen activa
82	429.5	21.1	429	2 A33309	uterine milk prote
83	428.5	21.1	464	1 XHHU3	antithrombin III p
84	428	21.0	379	2 S27383	elastase inhibitor
85	427.5	21.0	433	1 A61435	antithrombin III -
86	426	21.0	405	1 A41252	heat shock protein
87	424	20.9	465	2 I59611	antithrombin III -
88	423	20.8	213	2 A26423	serine proteinase
89	422.5	20.8	402	1 A34761	plasmaogen activa
90	422	20.8	418	2 A53120	intracellular coag
91	420	20.7	374	2 AH1903	hypothetical prote
92	420	20.7	418	2 A47281	pigment epithelial
93	414.5	20.4	431	1 JX0364	antithrombin III -
94	411	20.2	418	2 I52968	colligin-2 - human
95	410	20.2	359	2 D88940	protein C05E4.1 [i
96	406	20.0	359	2 A46046	serine proteinase
97	401.5	19.8	417	1 A40968	heat shock protein
98	401.5	19.8	417	1 A47222	uteroferin-associ
99	400.5	19.7	417	1 A42843	heat shock protein
100	399.5	19.7	417	1 S20608	heat shock protein

ALIGNMENTS

RESULT 1

ITHU

alpha-1-antitrypsin precursor [validated] - human
 N:Alternate names: alpha-1-AT; alpha-1-proteinase inhibitor
 C:Species: Homo sapiens (nan)
 C>Date: 30-Nov-1980 #sequence_revision 31-Mar-1992 #ext_change 09-Jul-2004
 C:Accession: A21853; B21853; A93352; A90944; A58528; A23174; A93281; A32336; S14476; A24
 R:Long, G.L.; Chandra, T.; Woo, S.L.C.; Davie, E.W.; Kurachi, K.
 Biochemistry 23, 4828-4837, 1984
 A:Title: Complete sequence of the cDNA for human alpha-1-antitrypsin and the gene for th
 A:Reference number: A21853; MUID:85047190; PMID:6093867
 A:Accession: A21853
 A:Molecule type: mRNA
 A:Residues: 1-287, 'V', 289-418 <LON2>
 A:Cross-references: GB:K02212; NID:G177830; PIDN:AAB59495.1; PID:G177831
 A:Experimental source: S variant allele
 R:Rosenberg, S.; Barr, P.J.; Najarian, R.C.; Hallowell, R.A.
 Nature 312, 77-80, 1984
 A:Title: Synthesis in yeast of a functional oxidation-resistant mutant of human alpha-1-
 A:Reference number: A93352; MUID:85036645; PMID:6387509
 A:Accession: A93352
 A:Molecule type: mRNA
 A:Residues: 1-124, 'H', 126-325, 'I', 327-418 <ROS>
 A:Cross-references: EMBL:X01683; NID:G28965
 R:Bollen, A.; Herzog, A.; Cravador, A.; Herion, P.; Chuchana, P.; Vander Straten, A.; Lo
 DNA 2, 255-264, 1983
 A:Title: Cloning and expression in Escherichia coli of full-length complementary DNA cod
 A:Reference number: A90944; MUID:84107980; PMID:6319097
 A:Accession: A90944
 A:Molecule type: mRNA
 A:Residues: 1-138, 'DG', 141-272, 'N', 274-418 <BOI>
 A:Cross-references: GB:K01396; NID:G28985
 A:Note: this sequence has been corrected in reference A58528
 R:Colau, B.; Chuchana, P.; Bollen, A.
 DNA 3, 327-330, 1984
 A:Title: Revised sequence of full-length complementary DNA coding for human alpha-1-anti
 A:Reference number: A58528; MUID:85026667; PMID:6333329
 A:Contents: Corrections to sequence in A90944
 A:Accession: A58528
 A:Molecule type: mRNA
 A:Residues: 1-418 <COL>
 A:Cross-references: GB:K01396; NID:G28965; PIDN:CAA25838.1; PID:G28966
 R:Cilberco, G.; Dente, L.; Cortese, R.
 Cell 41, 531-540, 1985
 A:Title: Cell-specific expression of a transfected human alpha-1-antitrypsin gene.
 A:Reference number: A23174; MUID:85176977; PMID:2985281
 A:Accession: A23174
 A:Molecule type: mRNA
 A:Residues: 1-11, 13-173, 'H', 175-228, 'D', 230-418 <CIL>
 A:Cross-references: GB:M11465; NID:G177826; PIDN:AA51546.1; PID:G177827
 A:Note: the authors state that this sequence corresponds to the M (normal) allele; 3 var
 R:Carrell, R.W.; Jeppsson, J.O.; Laurelli, C.B.; Brennan, S.O.; Owen, M.C.; Vaughan, L.;
 Nature 298, 329-334, 1982
 A:Title: Structure and variation of human alpha-1-antitrypsin.
 A:Reference number: A93281; MUID:82220135; PMID:7045697
 A:Accession: A93281
 A:Molecule type: protein
 A:Residues: 25-418 <CAR>
 A:Note: peptide sequence difference with A21853 (Leu-200 and the amidation states of re
 R:Zhu, X.J.; Kang, S.S.; Hargrove, K.; Shochat, D.; Jarrells, M.; Mojesky, M.; Chan, S.K
 Biochem. J. 246, 25-36, 1987
 A:Title: The identification of epitopic sites in human alpha-1-proteinase inhibitor.
 A:Reference number: A32336; MUID:88049621; PMID:2445337
 A:Accession: A32336
 A:Molecule type: protein

A:Residues: 25-418 <ZHU>
 A:Note: peptides were sequenced or partially sequenced and ordered by comparison with A21
 R:Weiland, K.L.; Falany, C.N.; Dooley, T.P.
 submitted to the EMBL Data Library, December 1989
 A:Description: Identification of a cDNA encoding a variant form of the human proteolytic
 A:Reference number: S14476
 A:Accession: S14476
 A:Molecule type: mRNA
 A:Residues: 142-230, 'V', 232-338 <WEI>
 A:Cross-references: EMBL:X17122; NID:G28636; PIDN:CAA34982.1; PID:G28637
 A:Experimental source: EMBL a variant form
 R:Riley, J.H.; Bathurst, I.C.; Edbrooke, M.R.; Carrell, R.W.; Craig, R.K.
 FEBS Lett. 189, 361-366, 1985
 A:Title: Alpha-1-antitrypsin and serum albumin mRNA accumulation in normal, acute phase
 A:Reference number: A24013; MUID:86005469; PMID:3876243
 A:Accession: A24013
 A:Molecule type: mRNA
 A:Residues: 292-418 <RIL>
 A:Cross-references: EMBL:X02920; NID:G24437; PIDN:CAA26677.1; PID:G24438
 R:Schulze, A.J.; Baumann, U.; Knof, S.; Jaeger, E.; Huber, R.; Laurelli, C.B.
 Eur. J. Biochem. 194, 51-56, 1990
 A:Title: Structural transition of alpha(1)-antitrypsin by a peptide sequentially similar
 A:Reference number: S13833; MUID:91071209; PMID:2253623
 A:Accession: S13833
 A:Molecule type: protein
 A:Residues: 25-41 <SCH>
 R:Niemann, W.A.; Narkates, A.J.; Miller, E.J.
 Matrix 12, 233-241, 1992
 A:Title: Isolation and serine protease inhibitory activity of the 44-residue, C-terminal
 A:Reference number: S23516; MUID:93024095; PMID:1406456
 A:Accession: S23516
 A:Molecule type: protein
 A:Residues: 375-409, 'L', 411-413, 'S' <NIE>
 R:Dengler, R.; Eger, G.; Lottspeich, F.; Plewan, A.; Ogilvie, A.; Emmerich, B.
 Biol. Chem. Hoppe-Seyler 373, 581-588, 1992
 A:Title: Proteolytic inactivation of alpha(1)-proteinase inhibitor in vivo: detection, c
 A:Reference number: S23962; MUID:92384968; PMID:1515087
 A:Accession: S23962
 A:Molecule type: protein
 A:Residues: 44-53;384-392 <DEN>
 R:Dengler, R.; Lottspeich, F.; Oberthuer, W.; Mast, A.E.; Emmerich, B.
 Biol. Chem. Hoppe-Seyler 376, 165-172, 1995
 A:Title: Limited proteolysis of alpha(1)-proteinase inhibitor (alpha(1)-PI) in acute leu
 A:Reference number: S55249; MUID:95336645; PMID:7612193
 A:Accession: S55249
 A:Molecule type: protein
 A:Residues: 25-28;43-47;207-208;382-389;414-418 <DE2>
 R:Leicht, M.; Long, G.L.; Chandra, T.; Kurachi, K.; Kidd, V.J.; Mace, M.
 Nature 297, 655-659, 1982
 A:Title: Sequence homology and structural comparison between the chromosomal human alpha
 A:Reference number: I39371; MUID:82220035; PMID:6979715
 A:Accession: I39371
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-67 <LEI1>
 A:Cross-references: GB:J00064; NID:G177817; PIDN:AAB59369.1; PID:G177822
 A:Accession: I39172
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 196-225 <LSI2>
 A:Cross-references: GB:J00066; NID:G177819; PIDN:AAB59370.1; PID:G177823
 R:Chang, W.S.W.; Wardell, M.R.; Lomas, D.A.; Carrell, R.W.
 Biochem. J. 314, 647-653, 1996
 A:Title: Probing serpin reactive-loop conformations by proteolytic cleavage.
 A:Reference number: S63599; MUID:96239126; PMID:8670081
 A:Accession: S63599
 A:Molecule type: protein
 A:Residues: 371-385 <CHA>
 R:Coutelle, C.; Speer, A.; Rogers, J.; Kalsheker, N.; Humphries, S.; Williamson, R.
 Biomed. Blochim. Acta 44, 421-431, 1985
 A:Title: Construction and partial characterization of a human liver cDNA library.
 A:Reference number: I39370; MUID:85225507; PMID:3873938
 A:Accession: I39370

A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 387-399, 'D', 401-418 <COU>
A;Cross-references: GB:M26123; NID:G177815; PIDN:AAA51545.1; PID:G177816
R;Faber, J.P.; Weidinger, S.; Olek, K.
Am. J. Hum. Genet. 46, 1158-1162, 1990
A;Title: Sequence data of the rare deficient alpha-1-antitrypsin variant PI Zausburg.
A;Reference number: A35338; MUID:90252805; PMID:23319709
A;Accession: A35338
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 122-124, 'H', 126-128, 363-365, 'K', 367-369 <FAB>
A;Experimental source: mutant PI Zausberg
A;Note: this Z mutation with Lys-366 arose from the M2 variant with His-125
R;Loebermann, H.; Tokuko, R.; Deisenhofer, J.; Huber, R.
submitted to the Brookhaven Protein Data Bank, September 1988
A;Reference number: A50775; PDB:7API
A;Contents: annotation: X-ray crystallography, 3.0 angstroms, tetragonal form 1, residue
R;Loebermann, H.; Tokuko, R.; Deisenhofer, J.; Huber, R.
submitted to the Brookhaven Protein Data Bank, September 1988
A;Reference number: A50794; PDB:8API
A;Contents: annotation: X-ray crystallography, 3.1 angstroms, hexagonal form, residues 4
R;Loebermann, H.; Tokuko, R.; Deisenhofer, J.; Huber, R.
submitted to the Brookhaven Protein Data Bank, September 1988
A;Reference number: A50810; PDB:9API
A;Contents: annotation: X-ray crystallography, 3.0 angstroms, tetragonal form 2, residue
R;Loebermann, H.; Tokuko, R.; Deisenhofer, J.; Huber, R.
J. Mol. Biol. 177, 531-556, 1984
A;Title: Human alpha-1-proteinase inhibitor. Crystal structure analysis of two crystal
A;Reference number: A58525; MUID:84292309; PMID:6332197
A;Contents: annotation: X-ray crystallography, 3.0 angstroms
R;Carrell, R.W.; Jeppsson, J.O.; Vaughan, L.; Brennan, S.O.; Owen, M.C.; Boswell, D.R.
FEBS Lett. 135, 301-303, 1981
A;Title: Human alpha-1-antitrypsin: carbohydrate attachment and sequence homology.
A;Reference number: A58526; MUID:82095611; PMID:6976274
A;Contents: annotation: carbohydrate attachment sites
C;Comment: The Z variant allele has Lys-366. Deficiency of the normal inhibitor in indivi
sis.
C;Genetics:
A;Gene: GDB:PI
A;Cross-references: GDB:120289; OMIM:107400
A;Map position: 14q32.1-14q32.1
A;Introns: 216/1; 306/2; 355/3
A;Note: the first intron occurs before the initiator codon
C;Function:
A;Description: inhibitor of serine proteinases, primarily leukocyte elastase and collagen
A;Note: it also inhibits plasmin, thrombin, kallikrein, trypsin, and chymotrypsin
C;Superfamily: Serpin
C;Keywords: acute phase; emphysema; glycoprotein; plasma; polymorphism; serine proteinase
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-418/Product: alpha-1-antitrypsin #status experimental <MAT>
F;70,107,271/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;382/Inhibitory site: Met (elastase, collagenase) #status experimental
Query Match 98.6%; Score 2003; DB 1; Length 418;
Best Local Similarity 98.5%; Pred. No. 2.8e-131;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 EDPOGDAAKTDTSHDQDHPFNKLTNPALAEFAPSLYQLAHQSNSTNIFPSPVSIATA 60
DB 25 EDPOGDAAKTDTSHDQDHPFNKLTNPALAEFAPSLYQLAHQSNSTNIFPSPVSIATA 84
QY 61 FAMLSTGTADTHDEILEGLNFNLTQIPRAQIHGEFQELLRTLNQDPSQLQLTGNGFL 120
DB 85 FAMLSTGTADTHDEILEGLNFNLTQIPRAQIHGEFQELLRTLNQDPSQLQLTGNGFL 144
QY 121 SQGLKLVDFLEVDKVLKLYHSEAFVNFQTEQAQKQINDYVEKGTQGIKIVDLVKELDRDT 180
DB 145 SEGLKLVDFLEVDKVLKLYHSEAFVNFQTEQAQKQINDYVEKGTQGIKIVDLVKELDRDT 204
QY 181 VFALVNYIFPKGWERPFVVKDTEEDFHVDDQVTTVKVPMKRLGMFNIOHCKKLSWVL 240
DB 205 VFALVNYIFPKGWERPFVVKDTEEDFHVDDQVTTVKVPMKRLGMFNIOHCKKLSWVL 264

QY 241 LMKYLGNAITAFPLPDEGKLQHLLENELTHDIIITKFLNEDRRSASLHLPKLSITGTVDLK 300
DB 265 LMKYLGNAITAFPLPDEGKLQHLLENELTHDIIITKFLNEDRRSASLHLPKLSITGTVDLK 324
QY 301 SVLGQIGITKVFSGADLSGVTEAPLKLKSKAVHKAVLTIDEKGTAAAGAMFLERIPRSI 360
DB 325 SVLGQIGITKVFSGADLSGVTEAPLKLKSKAVHKAVLTIDEKGTAAAGAMFLERIPMSI 384
QY 361 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPTQK 394
DB 385 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPTQK 418
RESULT 2
ITBA
N;Alternate names: alpha-1-proteinase precursor - baboon (fragment)
C;Species: Papio sp. (baboon)
C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 15-Sep-2003
R;Kurachi, K.; Chandra, T.; Degen, S.J.F.; White, T.T.; Marchioro, T.L.; Woo, S.L.C.; Day
Proc. Natl. Acad. Sci. U.S.A. 78, 6826-6830, 1981
A;Title: Cloning and sequence of cDNA coding for alpha-1-antitrypsin.
A;Reference number: A01248; MUID:82082539; PMID:7031661
A;Accession: A01248
A;Molecule type: mRNA
A;Residues: 1-409 <KUR>
A;Cross-references: GB:J00321; NID:G176561; PIDN:AAA53377.1; PID:G176562
C;Comment: Alpha-1-antitrypsin is an inhibitor of serine proteinases. Its primary target
psin.
C;Superfamily: Serpin
C;Keywords: acute phase; glycoprotein; plasma; serine proteinase inhibitor
F;1-15/Domain: signal sequence (fragment) #status predicted <SIG>
F;16-409/Product: alpha-1-antitrypsin #status predicted <MAT>
F;61,98,262/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;373/Inhibitory site: Met (elastase, collagenase) #status predicted
Query Match 92.0%; Score 1870; DB 1; Length 409;
Best Local Similarity 91.1%; Pred. No. 4.4e-122;
Matches 359; Conservative 21; Mismatches 14; Indels 0; Gaps 0;
QY 1 EDPOGDAAKTDTSHDQDHPFNKLTNPALAEFAPSLYQLAHQSNSTNIFPSPVSIATA 60
DB 16 EDPOGDAAKTDTSHDQDHPFNKLTNPALAEFAPSLYQLAHQSNSTNIFPSPVSIATA 75
QY 61 FAMLSTGTADTHDEILEGLNFNLTQIPRAQIHGEFQELLRTLNQDPSQLQLTGNGFL 120
DB 76 FAMLSTGTADTHDEILEGLNFNLTQIPRAQIHGEFQELLRTLNQDPSQLQLTGNGFL 135
QY 121 SQGLKLVDFLEVDKVLKLYHSEAFVNFQTEQAQKQINDYVEKGTQGIKIVDLVKELDRDT 180
DB 136 NKSLLKLVDFLEVDKVLKLYHSEAFVNFQTEQAQKQINDYVEKGTQGIKIVDLVKELDRDT 195
QY 181 VFALVNYIFPKGWERPFVVKDTEEDFHVDDQVTTVKVPMKRLGMFNIOHCKKLSWVL 240
DB 196 VFALVNYIFPKGWERPFVVKDTEEDFHVDDQVTTVKVPMKRLGMFNIOHCKKLSWVL 255
QY 241 LMKYLGNAITAFPLPDEGKLQHLLENELTHDIIITKFLNEDRRSASLHLPKLSITGTVDLK 300
DB 256 LMKYLGNAITAFPLPDEGKLQHLLENELTHDIIITKFLNEDRRSASLHLPKLSITGTVDLK 315
QY 301 SVLGQIGITKVFSGADLSGVTEAPLKLKSKAVHKAVLTIDEKGTAAAGAMFLERIPRSI 360
DB 316 TVLGHGIGITKVFSGADLSGVTEAPLKLKSKAVHKAVLTIDEKGTAAAGAMFLERIPMSI 375
QY 361 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPTQK 394
DB 376 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPTQK 409
RESULT 3
ITRT

A;Note: the authors translated the codon ATC for residue 395 as Ala
C;Comment: Alpha-1-antitrypsin is an inhibitor of serine proteinases. Its primary targeted psin.

C;Superfamily: Serpin
C;Keywords: acute phase; glycoprotein; plasma; serine proteinase inhibitor
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-416/Product: alpha-1-antitrypsin #status predicted <MAT>
F;58,105,269/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;380/Inhibitory site: Met (elastase, collagenase) #status predicted

Query Match 70.4%; Score 1430; DB 1; Length 416;
Best Local Similarity 69.2%; Pred. No. 1.4e-91;
Matches 269; Conservative 62; Mismatches 56; Indels 2; Gaps 1;

QY 4 QGDAAQKTDTHSHDQHPFTNKITPNLAEPFSLYRQLAHQSNSTNIFPSPVSIATAFAM 63
DB 28 QGHAVQETDDTSHQE--AACHKIAPNLANFAPSIYHHLAQSNSTNIFPSPVSIASAFAM 85
QY 64 LSLGTYADTHDELGLNPNLTQIPPAQIHGFEQELLRTLNQPDLSQQLTGTGNGLFSQ 123
DB 86 LSLGAKGNTHTEILGKLFNLTLEABAEIHKGPHLLHTLNQPNHQLTGTGNGLFINES 145
QY 124 LKLVDFLEDVKVLYHSEAFNFGDTEQAKKQINDYVEKGTGQKIVDLVKELDRDTVFA 183
DB 146 AKLVDTFLEDVKVLYHSEAFNFGDTEQAKKQINDYVEKGTGQKIVDLVKELDRDTVFA 205
QY 184 LNYIYFPKGRPEFVKDTEBEDFHVQDVTTVKVPMKRLGMFNIOHCKKLSWVLLMK 243
DB 206 LNYIYFPKGRPEFVKDTEBEDFHVQDVTTVKVPMKRLGMFNIOHCKKLSWVLLMK 265
QY 244 YLGNATAIFLPDEGKLOHLENLTHDIITKFLNEDRSASLHLPKLSITGYDLSV 303
DB 266 YVGNVTACFILPDGLKQLQLEDKLNELLAKFLEKKYASSANLHLPKLSITSETYDLK 325
QY 304 GOLGITYKVSNGADLSGVTEAPLKLKSAVHKAVLTIDEGTEAAGMFLERIPRIS 363
DB 326 GEIGINRVFSNGADLSGVTEAPLKLKSAVHKAVLTIDEGTEAAGMFLERIPRIS 385
QY 364 VKFNKPFVFLMIRQNTKSPFLFMGKVVNPT 392
DB 386 VEFNRPFLCILYDRNTKSPFLFMGKVVNPT 414

RESULT 6
S21097
alpha-1-antitrypsin precursor - bovine
N;Alternate names: alpha-1-proteinase inhibitor; proteinase inhibitor Inh3
C;Species: Bos primigenius taurus (cattle)
C;Date: 07-Apr-1994 #sequence_revision 19-May-1994 #text_change 09-Jul-2004
C;Accession: S21097; PC2040; S18920
R;Sinha, D.; Bakhehi, M.R.; Kirby, E.P.
Biochim. Biophys. Acta 1130, 209-212, 1992
A;Title: Complete cDNA sequence of bovine alpha-1-antitrypsin.
A;Reference number: S21097; MUID:922230396; PMID:1562597
A;Accession: S21097
A;Molecule type: mRNA
A;Residues: 1-416 <SIN>
A;Cross-references: UNIPROT:P34955; EMBL:X63129; NID:g41; PIDN:CAA44840.1; PID:g42
A;Note: the sequence from Fig. 2 is inconsistent with that from Fig. 1 in having 209-Thr
R;Sinha, D.; Yang, X.; Emig, F.; Kirby, E.P.
J. Biochem. 115, 387-391, 1994
A;Title: Isolation and characterization of two protease inhibitors from bovine plasma.
A;Reference number: PX0072; MUID:94334275; PMID:8056747
A;Accession: PC2040
A;Molecule type: protein
A;Residues: 25-44 <S12>
C;Superfamily: Serpin
C;Keywords: acute phase; glycoprotein; plasma; serine proteinase inhibitor
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-416/Product: alpha-1-antitrypsin #status predicted <MAT>
F;58,105,143,269/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 69.3%; Score 1409; DB 2; Length 416;

Best Local Similarity 68.4%; Pred. No. 4e-90;
Matches 266; Conservative 61; Mismatches 60; Indels 2; Gaps 1;

QY 4 QGDAAQKTDTHSHDQHPFTNKITPNLAEPFSLYRQLAHQSNSTNIFPSPVSIATAFAM 63
DB 28 QGHAVQETDDTSHQE--AACHKIAPNLANFAPSIYHHLAQSNSTNIFPSPVSIASAFAM 85
QY 64 LSLGTYADTHDELGLNPNLTQIPPAQIHGFEQELLRTLNQPDLSQQLTGTGNGLFSQ 123
DB 86 LSLGAKGNTHTEILGKLFNLTLEABAEIHKGPHLLHTLNQPNHQLTGTGNGLFINES 145
QY 124 LKLVDFLEDVKVLYHSEAFNFGDTEQAKKQINDYVEKGTGQKIVDLVKELDRDTVFA 183
DB 146 AKLVDTFLEDVKVLYHSEAFNFGDTEQAKKQINDYVEKGTGQKIVDLVKELDRDTVFA 205
QY 184 LNYIYFPKGRPEFVKDTEBEDFHVQDVTTVKVPMKRLGMFNIOHCKKLSWVLLMK 243
DB 206 LNYIYFPKGRPEFVKDTEBEDFHVQDVTTVKVPMKRLGMFNIOHCKKLSWVLLMK 265
QY 244 YLGNATAIFLPDEGKLOHLENLTHDIITKFLNEDRSASLHLPKLSITGYDLSV 303
DB 266 YVGNVTACFILPDGLKQLQLEDKLNELLAKFLEKKYASSANLHLPKLSITSETYDLK 325
QY 304 GOLGITYKVSNGADLSGVTEAPLKLKSAVHKAVLTIDEGTEAAGMFLERIPRIS 363
DB 326 GVGITVEFSRDLGSGITKQPLKVSALHKAALTIDEGTEAAGMFLERIPRIS 385
QY 364 VKFNKPFVFLMIRQNTKSPFLFMGKVVNPT 392
DB 386 VEFNRPFLCILYDRNTKSPFLFMGKVVNPT 414

RESULT 7
JX0346
alpha-1-antitrypsin precursor - Mongolian jird
C;Species: Meriones unguiculatus (Mongolian jird)
C;Date: 22-Apr-1995 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C;Accession: JX0346; PC2357
R;Goto, K.; Suzuki, Y.; Yoshida, K.; Yamamoto, K.; Sinohara, H.
J. Biochem. 116, 582-588, 1994
A;Title: Plasma alpha-1-antitrypsinase from the Mongolian gerbil, Meriones unguiculatus.
A;Reference number: JX0346; MUID:95155268; PMID:7852275
A;Accession: JX0346
A;Molecule type: mRNA
A;Residues: 1-406 <GOT>
A;Cross-references: UNIPROT:Q64118; GB:S77822; NID:g998663; PIDN:AAB33367.1; PID:g998664
A;Accession: PC2357
A;Molecule type: protein
A;Residues: 25-44; 77-96 <GO2>
A;Experimental source: plasma
C;Superfamily: Serpin
C;Keywords: glycoprotein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-406/Product: alpha-1-antitrypsinase #status predicted <MAT>
F;383-387/Region: serpin binding #status predicted
F;59,96,134,260,403/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;371/Inhibitory site: Met (trypsin, chymotrypsin, elastase) #status predicted

Query Match 66.5%; Score 1352; DB 2; Length 406;
Best Local Similarity 67.5%; Pred. No. 3.4e-86;
Matches 260; Conservative 58; Mismatches 61; Indels 6; Gaps 2;

QY 8 AOKTDTSHDQHPFTNKITPNLAEPFSLYRQLAHQSNSTNIFPSPVSIATAFAMLSUG 67
DB 27 AEKTDSSH--QDH-----INASNLADPAFGLYRVLSHQSNNTNIFLSPLSIATAMLSUG 80
QY 68 TKADTHDELGLNPNLTQIPPAQIHGFEQELLRTLNQPDLSQQLTGTGNGLFSQGLK 127
DB 81 SKDDTKAQLQLGLHFNLTETSEADIHKGPHLLKTLNRPDNEQLTGTGSLFVNNSLNV 140
QY 128 DKFLEDVKVLYHSEAFNFGDTEQAKKQINDYVEKGTGQKIVDLVKELDRDTVFA 187
DB 141 EKFLFEVKNHYHSEAFNFGDTEQAKKQINDYVEKGTGQKIVDLVKELDRDTVFA 200

QY	188	IFFGKWERPEVKDTEEDFHVQDVTTVKVPMMKRLGMENIOHCKKLSGWSVLLMKYLG	247
Db	201	IFFRGKWEKFPDELTEADFDYDKSTTVKVPMMNRGMFDVHYCDTLSSVLLMDYLG	260
QY	248	ATAIFLPDDEGKLOHLENELTHDIIITKFLNEDRRSASLHLPKLSITGTVDLKSIVLGQ	307
Db	261	ATAIFLPDDEGKQOHLQETLTKSHIYKFLQNRHTRGSANVHLPKLSISGTYNLKKVLSPLG	320
QY	308	ITKVFNSGADLSGVTEAPLKSVAHVKAULTIDEKGTAAAGAMFLERIPRSIPPEVKFN	367
Db	321	ITQVFSNGADLSGITDVPDLKSKAVHKAULTIDERGTEAAGTTVLEAVPMSIPPDVCFK	380
QY	368	KPVFLMIEONTKSPFLFMGKVVNPT	392
Db	381	NPFVVICDKHTQSPFLFVGKVVNPT	405
RESULT 8			
S54981			
alpha-1-antiproteinase isoform E precursor - rabbit			
C;Species: Oryctolagus cuniculus (domestic rabbit)			
C;Date: 28-Oct-1996 #sequence_revision 07-Feb-1997 #text_change 09-Jul-2004			
R;Accession: S54981; S72199			
R;Saito, A.; Sinohara, H.			
Biochem. J. 307, 369-375, 1995			
A;Title: Rabbit alpha-1-antiproteinase E: a novel recombinant serpin which does not inhibit			
A;Reference number: S54981; MUID:95251597; PMID:7733871			
A;Accession: S54981			
A;Molecule type: mRNA			
A;Residues: 1-413 <SA11>			
A;Cross-references: UNIPROT:Q28665; EMBL:D17725; NID:g1008927; PIDN:BA04579.1; PID:g100			
A;Accession: S72199			
A;Molecule type: protein			
A;Residues: 25-33;374-387 <SA12>			
C;Superfamily: Serpin			
C;Keywords: acute phase; emphysema; glycoprotein; plasma; serine proteinase inhibitor			
F;1-24/Domain: signal sequence #status predicted <SIG>			
F;25-413/Product: alpha-1-antiproteinase E #status experimental <MAT>			
Query Match 65.7%; Score 1335; DB 2; Length 413;			
Best Local Similarity 65.1%; Pred. No. 5.3e-85;			
Matches 252; Conservative 60; Mismatches 75; Indels 0; Gaps 0;			
QY	6	DAQKDTDTHDDHPTFNKIPNLAEPAFSLYROLAHQSNSTNIFFSPVSIATAFAMLS	65
Db	25	DEAQETAVSSEHQDHACHRIAPSLAEFALSRLREVAHESNTNIFFSPVSIATAFAMLS	84
QY	66	LGTADTHDEILGLNFLNLTQIPEAQIHGFOELLRLTLNQPSQLQTLTNGNGLFSLQGLK	125
Db	85	LGAKGDTHITQVLEGLKFNLTETAEAQIHGDFRLLHTVNRPDSELQALAAAGNALVVHENLK	144
QY	126	LVDKFLFEDVKVLVHSAFTVNGDTEQAQKQINDYVEKGTQGIQKIVDLVKELDRDTPFALV	185
Db	145	LQHKFLEDAKNLYQSEAFVDFRDPEQAKTKINSHVEKGTGRGKIVDLVOELDARTLLAV	204
QY	186	NYLFFGKWERPEVKDTEEDFHVQDVTTVKVPMMKRLGMENIOHCKKLSWVLLMKYL	245
Db	205	NYVFFGKWEKPEPENTKEEDFHVQATTVRVPMMSRLGMVNFHCSTLAVTLRNDYK	264
QY	246	GNATAIFFLPDEGKLOHLENELTHDIIITKFLNEDRRSASLHLPKLSITGTVDLKSIVLGQ	305
Db	265	GNATALFLLPDEGKLOHLEDTLTTELIAKFLAKLSRLSVTVRFPKLSISGTYNLKPLLG	324
QY	306	LGITKVFNSGADLSGVTEAPLKSVAHVKAULTIDEKGTAAAGAMFLERIPRSIPPEVK	365
Db	325	LGITQVFSNNADLSGITEQBPQKVSQALHKAULTIDERGTEAAGASFVELLIPESVPDSIT	384
QY	366	FNKPFVFLMIEONTKSPFLFMGKVVNPT	392
Db	385	LDRPFLFVIYSHEIKSPFLFVGKVVDP	411

RESULT 9			
I49470			
alpha-1 proteinase inhibitor 1 - mouse			
N;Alternate names: alpha-1-antitrypsin			
C;Species: Mus musculus (house mouse)			
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004			
R;Accession: I49470; A25495			
R;Borriello, F.; Krauter, K.S.			
Proc. Natl. Acad. Sci. U.S.A. 88, 9417-9421, 1991			
A;Title: Multiple murine alpha 1-protease inhibitor genes show unusual evolutionary diver			
A;Reference number: I49470; MUID:92052104; PMID:1946354			
A;Accession: I49470			
A;Status: preliminary; translated from GB/EMBL/DBJ			
A;Molecule type: mRNA			
A;Residues: 1-413 <RES>			
A;Cross-references: UNIPROT:P07758; GB:M75721; NID:g191841; PIDN:AAC28869.1; PID:g191842			
R;Krauter, K.S.; Citron, B.A.; Heu, M.T.; Powell, D.; Darnell Jr., J.E.			
DNA 5, 29-36, 1986			
A;Title: Isolation and characterization of the alpha-1-antitrypsin gene of mice.			
A;Reference number: A25495; MUID:86163765; PMID:3007061			
A;Accession: A25495			
A;Molecule type: mRNA			
A;Residues: 211-245; 'D', 247-322, 'L', 324-403, 'V', 405-413 <KRA>			
A;Cross-references: GB:M12586; NID:g192092; PIDN:AAA51624.1; PID:g192094			
C;Genetics:			
C;Gene: alpha-1 PI-1			
C;Superfamily: Serpin			
Query Match 65.3%; Score 1327; DB 2; Length 413;			
Best Local Similarity 64.1%; Pred. No. 1.9e-84;			
Matches 248; Conservative 70; Mismatches 67; Indels 2; Gaps 2;			
QY	9	OKTDTSHDDHPTFNKIPNLAEPAFSLYROLAHQSNSTNIFFSPVSIATAFAMLSLGT	68
Db	28	QETDTSQKQDS-PASHEIATNLGDFALSYRLVHQSNSTNIFFSPVSIATAFAMLSLGS	86
QY	69	KADTHDEILGLNFLNLTQIPEAQIHGFOELLRLTLNQPSQLQTLTNGNGLFSLQGLKLV	128
Db	87	KGDTHQIILEGLQFNLTQTSEADIHKSFOHLLQTLNRPDSELQSLSTGNGLFVNNDLKLVE	146
QY	129	KFLDVKVKKLYHSAFTVNGDTEQAQKQINDYVEKGTQGIQKIVDLVKELDRDTPFALVNY	188
Db	147	KFLSEAKNHYQAEVFSVNPFAESEAKKVINDFVEKGTQGIQKIAEAVKCLQDDTVFALANY	206
QY	189	FFGKWERPEVKDTEEDFHVQDVTTVKVPMMKRLGMENIOHCKKLSWVLLMKYLGNA	248
Db	207	LFKGKKKFPDENTEEAEFHVDESTTVKVPMMTSLGMLHVHHCSTLSSWVLLMDYAGNA	266
QY	249	TAIFFLPDDEGKLOHLENELTHDIIITKFLNEDRRSASLHLPKLSITGTVDLKSIVLGQ	308
Db	267	TAVFLLPDDGKQOHLQETLSKELSKFLNRRRLAQIHFPRLSISGEYNLKTLSPLGI	326
QY	309	TKVFSNGADLSGVTEB-APLKLKSAVHKAULTIDEKGTAAAGAMFLERIPRSIPPEVKFN	367
Db	327	TRIFNNGADLSGITEENAPFLKLSQAVHKAULTIDETGTAAAAVTVMQVPMSPMLTRFD	386
QY	368	KPVFLMIEONTKSPFLFMGKVVNPTGK	394
Db	387	HPFLFIIEHTQSPFLGKVVDPDTHK	413
RESULT 10			
JX0154			
alpha-1-antiproteinase F - rabbit			
C;Species: Oryctolagus cuniculus (domestic rabbit)			
C;Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 09-Jul-2004			
R;Accession: JX0154			
R;Saito, A.; Sinohara, H.			
J. Biochem. 109, 158-162, 1991			
A;Title: Cloning and sequencing of cDNA coding for rabbit alpha-1-antiproteinase F: amin			
A;Reference number: JX0154; MUID:91201273; PMID:2016265			
A;Accession: JX0154			
A;Status: preliminary			

A:Molecule type: mRNA
A:Residues: 1-413 <Sal>
A:Cross-references: UNIPROT:P23035; GB:X57710; NID:g1455; PIDN:CAA0881.1; PID:g1456
C:Superfamily: Serpin

Query Match 65.1%; Score 1322; DB 2; Length 413;
Best Local Similarity 64.3%; Pred. No. 4.2e-84;
Matches 249; Conservative 63; Mismatches 75; Indels 0; Gaps 0;

Qy 6 DAAQTDTSHHQDHPFNKITNLAEFAFSLYRQLAQHSNSTNIFFSPVSIATAFAMLS 65
Db ||| ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Qy 66 LGTKADTHDEILGELGNLNTQIPEAQIHGEFGQELLRTLNQPSQLQTTNGGLFLSQGLK 125
Db ||| ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Qy 85 LGAKGDHTTQVLEGLKENLTETAERAIHQDFGRHLLHTVNRPDSSELQAARNALVWHENLK 144
Db ||| ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Qy 126 LVQKFLEDVKKLHYHSEAFNTNFGTEOAKKOINDYVEKGTOGKIVDLAVKELDRDTPVALY 195
Db ||| ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Qy 145 LQHKLFLSDAKNLYOSEAPLVDFRDPQEAQKINSHVKEGRGKIVDVLUVELDARTLLAY 204
Db ||| ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Qy 186 NYIFFKGRWPFVFKVDTEBEDFHVDQVTTVKVPMKRRLGMFNIOHQCKLSSWVLLMKYL 245
Db ||| ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Qy 205 NYVFFKGWKPFPENTKEEDFHNATTVTRVPMSRLGRYDLFHCSTIASVLRMDYK 264
Db ||| ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Qy 246 GNATAIFPLPDEGKLQHLNELTHDIITKPLENEDRRSASLHLPKLSITCTYDLKSVLGQ 305
Db ||| ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Qy 265 GNATALPLL PDEGKLQHLEDTLTTELITKFLAKSSLRSVTVHPFKLSISGYDLKPLLGK 324
Db ||| ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Qy 306 LGITKVSNGADLSGVTEEARPKLSKAVHKAVLTIDEKGTGAAGMFLERI PRSIPPEVK 365
Db ||| ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Qy 325 LGITQVFSDNADLSGITQEQLKASQALHKAVALTIDERGTEAAGATYMEIIPMSLPDSIT 384
Db ||| ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Qy 366 FNKPFVLMTIEQNTKSPLFMGKVVNPT 392
Db ||| ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Qy 385 LDRPFLVIYSHEIKSPLFVGKVVDPPT 411
Db ||| ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||

RESULT 11
I49471
alpha-1 proteinase inhibitor 2 - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I49471
R:Borriello, F.; Krauter, K.S.
A>Title: Multiple murine alpha 1-protease inhibitor genes show unusual evolutionary divergence
A:Reference number: I49470; MUID:92052104; PMID:I4946354
A:Accession: I49471
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-402 <RES>
A:Cross-references: UNIPROT:P22599; GB:M75716; NID:g191843; PIDN:AAC28865.1; PID:g191844
C:Genetics:
A:Gene: alpha-1 PI-2
C:Superfamily: Serpin

Query Match 65.0%; Score 1321; DB 2; Length 402;
Best Local Similarity 64.1%; Pred. No. 4.7e-84;
Matches 248; Conservative 69; Mismatches 68; Indels 2; Gaps 2;

Qy 9 QKTDTSHHDQHPFNKITNLAEFAFSLYRQLAQHSNSTNIFFSPVSIATAFAMLSIGT 68
Db ||| ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Qy 17 QETDTSQKQAS-PASHEIATNLGDFALSRLVELVQSNTNIFFSPVSIATAFAMLSLGS 75
Db ||| ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Qy 69 KADTHDEILGELGNLNTQIPEAQIHGEFGQELLRTLNQPSQLQTTNGGLFLSQGLKLV 128
Db ||| ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Qy 76 KGDTHTTQILEGLQPNLTQTSADIHKSFQHLQTLNRPDSELQSLTNGGLFVNNDKLVE 135
Db ||| ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Qy 129 KFLEDVKKLHYHSEAFNTNFGTEOAKKOINDYVEKGTOGKIVDLVYKELDRDTPVALYNI 188
Db ||| ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Qy 136 KFLFEAKNHYYQAEVFSVNFASEEAKVINDFVEKGTQGKIVEAVKELDDQTVTVALANYI 195
Db ||| ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||

Db 327 TRIFNCGADLSGITEENAPLKLKAVHKAVLTIDETCTEAAAATVLQVATYSMPPIVRED 386

Qy 368 KPFVFLMIEONTKSPFLPMGKVNPTGK 394

Db 387 HPFLFIIFEHTQSPIFVGVKVDPTHK 413

Search completed: June 20, 2005, 19:46:41
Job time : 45 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2005, 19:34:59 ; Search time 172 Seconds
(without alignments)
1173.019 Million cell updates/sec

Title: PDX1
Perfect score: 2032
Sequence: 1 EDPQDAQKTSTSHDQDH.....IEQNTKSPFMGKVNPTCK 394

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : UniProt 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	DB ID	Description
1	2003	98.6	418	1 ALAT HUMAN
2	1883	92.7	396	2 O00394
3	1870	92.0	409	1 ALAT PAPAN
4	1701	83.7	370	2 Q86U18
5	1472.5	72.5	412	1 ALAT CALCN
6	1462	71.9	309	2 Q86U19
7	1459.5	71.8	421	1 ALAT PIG
8	1458	71.8	413	2 O54761
9	1443.5	71.0	411	1 ALAT RAT
10	1443.5	71.0	411	2 Q6AYZ5
11	1440.5	70.9	421	2 O46519
12	1431.5	70.4	413	2 P97277
13	1430	70.4	416	1 ALAT SHEEP
14	1427	70.2	413	1 ALMT TMSI
15	1414	69.6	413	2 Q76HP0
16	1409	69.3	416	1 ALAT BOVIN
17	1383	68.1	413	1 ALST TMSI
18	1379	67.9	413	1 ALST TMSI
19	1372	67.5	413	2 Q76HN9
20	1362	67.0	413	1 ALMS TMSI
21	1352	66.5	406	2 Q64118
22	1335	65.7	413	2 Q28665
23	1327	65.3	413	1 A1T1 MOUSE
24	1327	65.3	413	2 Q8VC20
25	1327	65.3	413	2 Q76HP1
26	1326	65.3	410	2 Q91V74
27	1326	65.3	413	2 Q91XB8
28	1326	65.3	413	2 Q91XB8
29	1326	65.3	422	2 Q80YB8
30	1322	65.1	413	1 ALAF RABIT
31	1322	65.1	425	2 Q91XCI

32	1321	65.0	413	1 ALT3 MOUSE
33	1320	65.0	413	1 ALT2 MOUSE
34	1316	64.8	413	2 Q8VC41
35	1315	64.7	413	2 Q07298
36	1314	64.7	456	2 O62663
37	1310	64.5	413	1 ALT4 MOUSE
38	1301	64.0	413	1 HP55-TMSI
39	1298	63.9	413	2 Q28666
40	1296	63.8	413	2 Q63969
41	1294	63.7	413	1 ALT5 MOUSE
42	1281.5	63.1	412	1 ALAT MUCR
43	1280	63.0	405	1 ALAS-CAVPO
44	1280	63.0	413	2 O54762
45	1260	62.0	403	1 ALAF-CAVPO
46	1235	60.8	410	1 COTR-CAVPO
47	1168	57.5	413	2 Q91X22
48	1153.5	56.8	410	1 ALAT DIDMA
49	1125	55.4	420	1 ALAU HUMAN
50	1012	49.8	433	2 Q9Y1B8
51	1007.5	49.6	432	2 Q7SYX0
52	1004	49.4	197	2 Q13747
53	1001	49.3	431	2 Q66KX6
54	946	46.6	426	2 Q8JIA6
55	839.5	41.3	420	2 Q60552
56	834	41.0	410	2 Q90323
57	833	41.0	407	2 Q9UNU9
58	833	41.0	423	1 AACT HUMAN
59	829	40.8	406	1 IPSP HUMAN
60	828	40.7	411	2 Q9TTE1
61	824	40.6	418	1 COTR MOUSE
62	824	40.6	418	2 Q91X80
63	823	40.5	418	2 Q8VCH3
64	822	40.5	418	2 Q03734
65	821.5	40.4	415	2 Q9GMA6
66	820	40.4	418	2 Q91W80
67	819	40.3	427	1 KAIN HUMAN
68	819	40.3	445	2 Q85TR9
69	813.5	40.0	416	2 Q6P6G8
70	813.5	40.0	426	2 Q72ZW1
71	813	40.0	435	2 Q6P519
72	811.5	39.9	405	1 CBG HUMAN
73	810.5	39.9	405	2 Q72ZQ9
74	807	39.7	418	2 Q62257
75	806	39.7	406	1 CBG SAISC
76	804.5	39.6	416	1 CPI1 RAT
77	804.5	39.6	418	2 Q91WP6
78	804	39.6	383	1 CBG RABIT
79	804	39.6	440	2 Q85U17
80	803.5	39.5	418	2 Q62258
81	803	39.5	418	1 CPI6 RAT
82	802	39.5	413	1 CPI3 RAT
83	797	39.2	430	1 CBG SHEEP
84	796.5	39.2	412	1 THBG PIG
85	795	39.1	404	2 Q9N2I2
86	793	39.0	417	1 KBP MOUSE
87	791	38.9	414	2 Q81W75
88	788.5	38.8	418	1 THBG SHEEP
89	786.5	38.7	412	1 THBG SHOE
90	783	38.5	471	2 Q80X76
91	782.5	38.5	411	1 THBG BOVIN
92	781.5	38.5	415	1 THBG HUMAN
93	780.5	38.4	405	1 IPSP MOUSE
94	776.5	38.2	415	1 THBG PANTR
95	775.5	38.2	406	2 Q88292
96	772.5	38.0	406	2 Q66HL5
97	771.5	38.0	418	1 SI24 APOSY
98	771.5	38.0	418	1 THBG RAT
99	767.5	37.8	405	2 Q8BU50
100	765.5	37.7	424	2 Q8CIE0

ALIGNMENTS

RESULT 1
 ALIAT HUMAN STANDARD; PRT; 418 AA.
 AC F01009; Q13672; Q96BF9; Q96ES1; Q9F1P0;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Alpha-1-antitrypsin precursor (Alpha-1 protease inhibitor) (Alpha-1-
 antitrypsinase) (PRO684/PRO2209).
 GN Names:SERPINAI; Synonyms=AAT, Pi;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
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 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
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 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Smallos D.E.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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QY 181 VFALVNYIFFKQKWERPFVEKDTSEDFHVDQVTTVKVPMKRLGMFNIQHCKKLSWWL 240
Db 183 VFALVNYIFFKQKWERPFVEATKEBDFHVDQATTVKVPMRRLGMFNIYHCKKLSWWL 242
QY 241 LMKYLGNAITAFPLPDEGKQHLLENELTHDITTKFLENEDRRSASLHLPKLSITGTYYDLK 300
Db 243 LMKYLGNAITAFPLPDEGKQHLLENELTHDITTKFLENENRRSANLHLPKLAITGTYYDLK 302
QY 301 SVLGQLGITKVFSGNGADLSGVTEAPLKLKSKAVHKAVALTIDKGTAAAGAMFLERIPRSI 360
Db 303 TVLGHGKITKVFSGNGADLSGVTEADAPLKLKSKAVHKAVALTIDKGTAAAGAMFLERIPRSI 362
QY 361 PPEVKFNKPFVFLMIEQNTKSPLEFMGKVVNPQK 394
Db 363 PPEVKFNKPFVFLMIEQNTKSPLEFMGKVVNPQK 396

RESULT 3
ALAT_PAPAN STANDARD; PRT; 409 AA.
AC P01010;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE Alpha-1-antitrypsin precursor (Alpha-1 protease inhibitor) (Alpha-1-
DE antiprotease) (AAT) (Fragment).
GN Names=SERPIN1; Synonyms=PI;
OS Papio anubis (olive baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheinae; Papio.
OX NCBI_TaxID=9555;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82082539; PubMed=7031661;
RA Kurchi K., Chandra T., Friezen Degen S.J., White T.T.,
RA Marchioro T.L., Woo S.L.C., Davie E.W.;
RT "Cloning and sequence of cDNA coding for alpha 1-antitrypsin.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:6826-6830(1981).
CC -!- FUNCTION: Inhibitor of serine proteases. Its primary target is
CC elastase, but it also has a moderate affinity for plasmin and
CC thrombin.
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- TISSUE SPECIFICITY: Plasma.
CC -!- SIMILARITY: Belongs to the serpin family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; J00321; AAA35377.1; -.
DR HSSP; P01009; 1EZX.
DR InterPro; IPR000215; Prot_inh_serpin.
DR Pfam; PF00079; Serpin; 1.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; 1.
KW Acute phase; Glycoprotein; Plasma; Serine protease inhibitor; Serpin;
KW Signal.
FT NON_TER 1 1
FT SIGNAL <1 15
FT CHAIN 16 409 Alpha-1-antitrypsin.
FT SITE 373 374 Reactive bond.
FT CARBOHYD 61 61 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 98 98 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 136 136 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 262 262 N-linked (GlcNAc... ) (Potential).
SQ SEQUENCE 409 AA; 45694 MW; E1980B7450FDBA9B CRC64;

Query Match 92.0%; Score 1870; DB 1; Length 409;
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Best Local Similarity 91.1%; Pred. No. 2.5e-116;
Matches 359; Conservative 21; Mismatches 14; Indels 0; Gaps 0;

QY 1 EDPQDAAQKTDTSHHDDQDHPFNKITPNLAFAFSLYQLAHQSNSTNIFSPVSIATA 60
Db 16 EDPQDAAQKTDTPPHDQNHPTLNKITPSLAFAFSLYQLAHQSNSTNIFSPVSIATA 75
QY 61 FAMLISGTKADTHDEILEGINFNLTQIPRAQIHEGFQELLRTLNOPDSQLQTTGNGLFL 120
Db 76 FAMLISGTKADTHSELGLNFNLTEIPEAQVHEGFQELLRTLNKPEDSQLQTTGNGLFL 135
QY 121 SGLKLVDKFLPDEVKLYHSEAFNTNFGTEQAQKQINDYVEKGTQGKIYDLVKELDRDT 180
Db 136 NKSLKVDKFLPDEVKLYHSEAFNVNFEDTEBAKQINNYVEKGTQGVVLDVKELDRDT 195
QY 181 VFALVNYIFFKQKWERPFVEKDTSEDFHVDQVTTVKVPMKRLGMFNIQHCKKLSWWL 240
Db 196 VFALVNYIFFKQKWERPFVEATEBEDFHDQATTVKVPMRRLGMFNIYHCKKLSWWL 255
QY 241 LMKYLGNAITAFPLPDEGKQHLLENELTHDITTKFLENEDRRSASLHLPKLSITGTYYDLK 300
Db 256 LMKYLGNAITAFPLPDEGKQHLLENELTHDITTKFLENENRRSANLHLPKLAITGTYYDLK 315
QY 301 SVLGQLGITKVFSGNGADLSGVTEAPLKLKSKAVHKAVALTIDKGTAAAGAMFLERIPRSI 360
Db 316 TVLGHGKITKVFSGNGADLSGVTEADAPLKLKSKAVHKAVALTIDKGTAAAGAMFLERIPRSI 375
QY 361 PPEVKFNKPFVFLMIEQNTKSPLEFMGKVVNPQK 394
Db 376 PPEVKFNKPFVFLMIEQNTKSPLEFMGKVVNPQK 409

RESULT 4
Q85U18 PRELIMINARY; PRT; 370 AA.
AC Q86U18;
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Full-length cDNA clone CS0DM003YH14 of Fetal liver of Homo sapiens
DE (human) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal liver;
RA Li W.B., Gruber C., Jessee J., Polayes D.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal liver;
RA Genoscope;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the serpin family.
DR EMBL; BX248257; CAD62585.1; -.
DR HSSP; P01009; 8API.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR000215; Prot_inh_serpin.
DR Pfam; PF00079; Serpin; 1.
DR SMART; SM00093; SERPIN; 1.
KW Protease inhibitor; Serine protease inhibitor; Serpin.
FT NON_TER 1 1
SQ SEQUENCE 370 AA; 41448 MW; 024F8B34B600E204 CRC64;

Query Match 83.7%; Score 1701; DB 2; Length 370;
Best Local Similarity 99.1%; Pred. No. 3.8e-105;
Matches 328; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDPQDAAQKTDTSHHDDQDHPFNKITPNLAFAFSLYQLAHQSNSTNIFSPVSIATA 60
Db 36 EDPQDAAQKTDTSHHDDQDHPFNKITPNLAFAFSLYQLAHQSNSTNIFSPVSIATA 95
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QY 61 FAMSLSGKTADTHDEILLEGLENFNLTQIPERAIHEGFQELLRTLNQPPDSQLQLTGNGLFL 120
 DB 96 FAMSLSGKTADTHDEILLEGLENFNLTQIPERAIHEGFQELLRTLNQPPDSQLQLTGNGLFL 155
 QY 121 SOGLKLVDFKLEVDVKLYHSEAFVNFQDTEQAKQINDYVEKGTQGIKIVDLVKELDRDT 180
 DB 156 SEGKLVDFKLEVDVKLYHSEAFVNFQDTEQAKQINDYVEKGTQGIKIVDLVKELDRDT 215
 QY 181 VFALVNYIFPKGKWERPFVEKDTSEEDFHVQDVTTKVPMKRLGMFNIQHCKKLSWVL 240
 DB 216 VFALVNYIFPKGKWERPFVEKDTSEEDFHVQDVTTKVPMKRLGMFNIQHCKKLSWVL 275
 QY 241 LMKYLGNATAIFLDPBEGKLOHLENELTHDIITKFLNEDRRSASLHLPKLSITGYVDLK 300
 DB 276 LMKYLGNATAIFLDPBEGKLOHLENELTHDIITKFLNEDRRSASLHLPKLSITGYVDLK 335
 QY 301 SVLGQGITKVFSGNADLSGVTEAPLKLSK 331
 DB 336 SVLGQGITKVFSGNADLSGVTEAPLKLSK 366

RESULT 5
 ALAT CALCN STANDARD; PRT; 412 AA.
 AC Q54763;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Alpha-1-antitrypsinase precursor (Alpha-1-antitrypsin) (Alpha-1-
 proteinase inhibitor).
 DE Callosclurus caniceps (Gray-bellied squirrel).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Scuridae; Scurinae;
 OC Callosclurus.
 OX NCBI_TaxID=64664;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=98094263; PubMed=9431474; DOI=10.1016/S0378-1119(97)00532-5;
 RA Takamatsu N., Kojima M., Taniyama M., Ohba K., Uematsu T., Segawa C.,
 Teutou S., Watanabe M., Kondo J., Kondo N., Shiba T.;
 RT "Expression of multiple alpha-1-antitrypsin-like genes in hibernating
 species of the squirrel family.";
 RL Gene 204:127-132(1997).
 CC -1- FUNCTION: Inhibitor of serine proteases (By similarity).
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: Plasma.
 CC -1- SIMILARITY: Belongs to the serpin family.

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 or send an email to license@ebi.ac.uk).

 DR EMBL; AB000552; BAA24422.1; -.
 DR HSSP; P01009; IQMB.
 DR InterPro; IPR000215; Prot_inh_serpin.
 DR Pfam; PF000079; Serpin; 1.
 DR SMART; SM00093; SERPIN; 1.
 DR PROSITE; PS00284; SERPIN; 1.
 KW Acute phase; Glycoprotein; Plasma; Serine protease inhibitor; Serpin;
 Signal.
 FT SIGNAL 1 24 Potential.
 FT CHAIN 25 412 Alpha-1-antitrypsinase.
 FT SITE 377 378 Reactive bond (By similarity).
 FT CARBOHYD 65 65 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 102 102 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 165 165 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 266 266 N-linked (GlcNAc...) (Potential).

SQ SEQUENCE 412 AA; 45729 MW; 7235668E9EB8FCC6 CRC64;
 Query Match 72.5%; Score 1472.5; DB 1; Length 412;
 Best Local Similarity 72.7%; Pred. No. 7.2e-90;
 Matches 282; Conservative 46; Mismatches 59; Indels 1; Gaps 1;
 QY 5 GDAQAQKDTSHHDQDPTNKITPNLAEPAFSLYRQLAHQSNTNIFFSVSTATAFAML 64
 DB 25 GD-AQETDASAKDHEHPACHKIAPNLAEFAFDLYRLARQSNNTNIFFSVSTATAFAML 83
 QY 65 SLGKTADTHDEILLEGLENFNLTQIPERAIHEGFQELLRTLNQPPDSQLQLTGNGLFLSOGL 124
 DB 84 SLGKTADTHDEILLEGLENFNLTQIPERAIHEGFQELLRTLNQPPDSQLQLTGNGLFLSOGL 143
 QY 125 KLVDKLEVDVKLYHSEAFVNFQDTEQAKQINDYVEKGTQGIKIVDLVKELDRDTVPAL 184
 DB 144 KLADKLEVDVKLYHSEAFVNFQDTEQAKQINDYVEKGTQGIKIVDLVKELDRDTVPAL 203
 QY 185 VNYIFPKGKWERPFVEKDTSEEDFHVQDVTTKVPMKRLGMFNIQHCKKLSWVLMMKY 244
 DB 204 VNYIFPKGKWERPFVEKDTSEEDFHVQDVTTKVPMKRLGMFNIQHCKKLSWVLMMKY 263
 QY 245 LGNATAIFLDPBEGKLOHLENELTHDIITKFLNEDRRSASLHLPKLSITGYVDLKSVLG 304
 DB 264 LGNATAIFLDPBEGKLOHLENELTHDIITKFLNEDRRSASLHLPKLSITGYVDLKSVLG 323
 QY 305 QLGITKVFSGNADLSGVTEAPLKLSKAVHKAIVLITDERGTEAAGAMFLERIPRSIPPEV 364
 DB 324 TLGITKVFSGNADLSGVTEAPLKLSKAVHKAIVLITDERGTEAAGAMFLERIPRSIPPEV 383
 QY 365 KFNKPFVFLMIEQNTKSPFMKGVNPT 392
 DB 384 RFDRLPLIIHYHYTKSPFLFVGKVNPT 411

RESULT 6
 Q86U19 PRELIMINARY; PRT; 309 AA.
 AC Q86U19;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Full-length cDNA clone CS0DM003YH10 of fetal liver of Homo sapiens
 (human) (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Fetal liver;
 RA Li W.B., Gruber C., Jesse J., Polayes D.;
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Fetal liver;
 RA Genoscope;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the serpin family.
 DR EMBL; BX248002; CAD62334.1; -.
 DR HSSP; P01009; BAPI.
 DR GO; GO:004867; F:serine-type endopeptidase inhibitor activity; IEA.
 DR InterPro; IPR000215; Prot_inh_serpin.
 DR Pfam; PF00079; Serpin; 1.
 DR SMART; SM00093; SERPIN; 1.
 KW Protease inhibitor; Serine protease inhibitor; Serpin.
 FT NON_TER 1
 SQ SEQUENCE 309 AA; 35116 MW; 5AF00026C06FBE9E CRC64;
 Query Match 71.9%; Score 1462; DB 2; Length 309;
 Best Local Similarity 98.9%; Pred. No. 2.5e-89;
 Matches 279; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 EDPOGDAQAQKTDTSRHHDDQDHPFNKITPNLAEPFAFSLYRQLAHQSNSTNIFPSPVSIATA 60
Db 28 EDPOGDAQAQKTDTSRHHDDQDHPFNKITPNLAEPFAFSLYRQLAHQSNSTNIFPSPVSIATA 87
QY 61 FAMLISGTTKADTHDEILEGLNFNLTQIPRAQIHGEGFQELLRTLNQPDQSOLQTLTNGNLF 120
Db 88 FAMLISGTTKADTHDEILEGLNFNLTQIPRAQIHGEGFQELLRTLNQPDQSOLQTLTNGNLF 147
QY 121 SOGLKLVDFLEDDVKLYHSEAFVNFNGTEQAKQINDYVEKGTQCKIVDLVKELDRDT 180
Db 148 SEGKLVDFLEDDVKLYHSEAFVNFNGTEQAKQINDYVEKGTQCKIVDLVKELDRDT 207
QY 181 VFALVNYIIFKKGWERPFVKDTEEDFHVQDVTVTKVPMKRLGFMFNIOHCKKLSWYL 240
Db 208 VFALVNYIIFKKGWERPFVKDTEEDFHVQDVTVTKVPMKRLGFMFNIOHCKKLSWYL 267
QY 241 LMKYLGNAITAFPLPDEGKLOHLENELTHDIIITKFLFLENEDRR 282
Db 268 LMKYLGNAITAFPLPDEGKLOHLENELTHDIIITKFLFLENEDRR 309

RESULT 7
ALAT_PIG STANDARD; PRT; 421 AA.
AC P50447;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Alpha-1-antitrypsin precursor (Alpha-1 protease inhibitor) (Alpha-1-
DE antiprotease).
GN Name=SERPIN1; Synonyms=PI;
OS Sus scrofa (Pig).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=97009792; PubMed=8856896;
RA Archibald A.L., Couperwhite S., Mellink C.H.M., Lahbib-Mansais Y.,
RA Gellin J.;
RT "Porcine alpha-1-antitrypsin (PI): cDNA sequence, polymorphism and
RT assignment to chromosome 7q2.4-q2.6.";
RL Anim. Genet. 27:85-89(1996).
CC -I- FUNCTION: Inhibitor of serine proteases. Its primary target is
CC elastase, but it also has a moderate affinity for plasmin and
CC thrombin (by similarity).
CC -I- SUBCELLULAR LOCATION: Extracellular.
CC -I- SIMILARITY: Belongs to the serpin family.
CC -----
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CC -----
DR EMBL; X88780; CAA61259.1; -.
DR HSSP; P01009; 1QMB.
DR InterPro; IPR000215; Prot_inh_serpin.
DR Pfam; PF00079; Serpin; 1.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; 1.
KW Glycoprotein; Plasma; Serine protease inhibitor; Serpin; Signal.
FT SIGNAL 1 24 Potential.
FT CHAIN 25 421 Alpha-1-antitrypsin.
FT SITE 385 386 Reactive bond.
FT CARBOHYD 73 73 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 110 110 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 421 AA; 47194 MW; 08A4AB2A95E60690 CRC64;

Query Match 71.8%; Score 1459.5; DB 1; Length 421;
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Best Local Similarity 72.0%; Pred. No. 5.4e-89;
Matches 286; Conservative 40; Mismatches 68; Indels 3; Gaps 1;

QY 1 EDPOGDAQAQKTDTSRHHDDQDHPFNKITPNLAEPFAFSLYRQLAHQSNSTNIFPSPVSI 57
Db 25 EGLQGHAVQETDPRHDHEHQHQAACHRIAPNLADFAFSLYRQVARQSNISIFLSPVTI 84
QY 58 ATAFAMLSIGTGTADTHDEILEGLNFNLTQIPRAQIHGEGFQELLRTLNQPDQSOLQTLTNG 117
Db 85 ARAFAMLSIGTGTAGATHAEILEGLQFNLTAKAEAEIHGEGFQHLHTLNQPDNLQTLTNG 144
QY 118 LFLSOGKLVDFLEDDVKLYHSEAFVNFNGTEQAKQINDYVEKGTQCKIVDLVKELD 177
Db 145 LPIDEKAKLVDFLEDDVKLYHSEAFVNFNGTEQAKQINDYVEKGTQCKIVDLVKELD 204
QY 178 RDTVFALVNYIIFKKGWERPFVKDTEEDFHVQDVTVTKVPMKRLGFMFNIOHCKKLS 237
Db 205 KDTVFALVNYIIFKKGWERPFVKDTEEDFHVQDVTVTKVPMKRLGFMFNIOHCKKLS 264
QY 238 WYLLMKYLGNAITAFPLPDEGKLOHLENELTHDIIITKFLFLENEDRRSASLHLPKLSITGY 297
Db 265 WYLLMDYVATATAFFILPDQGKLHQLQEDMLTKAIRAKPLEKRYPPSSANLHLPKLSITGY 324
QY 298 DLKSVLGQLGITKVPFSGADLSGVTEAPLKLKSKAVHKAVALIIDKGTGAAGAMFLERIP 357
Db 325 DLKSLGLNGLGITKVPFSGADLSGVTEAPLKLKSKALHRAVLTIIDEKGTGATGATILEAIP 384
QY 358 RSIPPEVFNKPFVFLMTIQNTKSPLEMGKVNPTGK 394
Db 385 MSIPPNVFNKPFVFLMTIQNTKSPLEMGKVNPTGK 421

RESULT 8
O54761 PRELIMINARY; PRT; 413 AA.
AC O54761;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Alpha-antitrypsin-like protein.
OS Spemophilus tridecemlineatus (Thirteen-lined ground squirrel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Scuriuridae; Sciurinae;
OC Spemophilus.
OX NCBI_TaxID=43179;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=98094263; PubMed=9434174; DOI=10.1016/S0378-1119(97)00532-5;
RA Takamatsu N., Kojima M., Taniyama M., Ohba K., Uematsu T., Segawa C.,
RA Tautou S., Watanabe M., Kondo J., Kondo N., Shiba T.;
RT "Expression of multiple alaphal-antitrypsin-like genes in hibernating
RT species of the squirrel family.";
RL Gene 204:127-132(1997).
CC -I- SIMILARITY: Belongs to the serpin family.
DR EMBL; AB000550; BAA24420.1; -.
DR HSSP; P01009; 1QMB.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR000215; Prot_inh_serpin.
DR Pfam; PF00079; Serpin; 1.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; 1.
KW Protease inhibitor; Serine protease inhibitor; Serpin.
SQ SEQUENCE 413 AA; 45953 MW; B08D2544695EE0F4 CRC64;

Query Match 71.8%; Score 1458; DB 2; Length 413;
Best Local Similarity 71.2%; Pred. No. 6.6e-89;
Matches 274; Conservative 56; Mismatches 55; Indels 0; Gaps 0;

QY 8 AOKTDTSHDDQDHPFNKITPNLAEPFAFSLYRQLAHQSNSTNIFPSPVSIATFAMLSLG 67
Db 27 AOKTGSKHDQHPASHRIAPNLAEFALSLYRVLAEHSNTNIFPSPVSIATFAMLSLG 86
```

QY 68 TKADTHDEILGLNPNLTQIPRAQIHGSPQELLTLNOPSOLQTLTGNGFLSOGKLV 127
 DB 87 TKADTHQIIMEGLGFLNLTAEASIHQSPQELLTLNOPSOLQTLTGNGFLSOGKLV 146
 QY 128 DKFLDVKLYHSAFTWFGDTEQAOKQINDVVEKGTQKQIVDLVKELDRDTVFALVY 187
 DB 147 DKFLQDVKNLYHSAFTDNTTAEAKQINTVVEKGTQKQIVDLVKELDRDVSVALVY 206
 QY 188 IFPGKWERPFEVKOTBEEDFHVQDVQVTVKVPMMKRLGMFNIQHCCKLSSWVLLMKYLG 247
 DB 207 IFPGKWERPFEVKOTBEEDFHVQDVQVTVKVPMMKRLGMFNIQHCCKLSSWVLLMKYLG 266
 QY 248 ATAIFPLPDGKLOHLENELTHDIITKFLNEDRSASLHLPKLSITGTYDLKSVLGQIG 307
 DB 267 ATAIFLLPDGKLOHLEDDITKFLAKFLKRRSSVNLHFPKLSITGTYDLKSVLTRLG 326
 QY 308 ITKVFSGADLSGVTEAPLKLKSAVHKAVLTIDKGTGAAGAMFLERIPRSPPEVKFN 367
 DB 327 ITNVFSYKADLSGITEEDPLRVQALHKAVALTIDERGTEAAGATFLEMMPSPPEVKFD 386
 QY 368 KPFVFLMIEQNTKSPPLFMGKVNP 392
 DB 387 KPFLVWIIHSTKSPPLFVGKVNP 411

RESULT 9

ALAT_RAT STANDARD; PRT; 411 AA.
 AC PL1475;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Alpha-1-antitrypsin precursor (Alpha-1-antitrypsin) (Alpha-1-
 DE proteinase inhibitor).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=101116;
 RN [1]
 RP SEQUENCE OF 4-411 FROM N.A., AND SEQUENCE OF 25-57.
 RC TISSUE=Liver;
 RX MEDLINE=90148955; PubMed=2302382;
 RA Chao S., Chai K.X., Chao L., Chao J.;
 RT "Molecular cloning and primary structure of rat alpha 1-antitrypsin.";
 RL Biochemistry 29:323-329(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar; TISSUE=Liver;
 RX MEDLINE=91035351; PubMed=2229024;
 RA Misumi Y., Sohda M., Ohkubo K., Takami N., Oda K., Ikehara Y.;
 RT "Molecular cloning and sequencing of the cDNA of rat alpha 1-protease
 RT inhibitor and its expression in COS-1 cells.";
 RL J. Biochem. 108:230-234(1990).
 RN [3]
 RP SEQUENCE OF 188-389 FROM N.A.
 RC TISSUE=Liver;
 RA Flink I.L., Bailey T., Morkin E.;
 RL Submitted (AUG-1989) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: Inhibitor of serine proteases. The primary target is
 CC elastase, but also has a moderate affinity for plasmin and
 CC thrombin.

CC -1- SUBCELLULAR LOCATION: Extracellular.

CC -1- TISSUE SPECIFICITY: Plasma.

CC -1- SIMILARITY: Belongs to the serpin family.

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CC

DR EMBL; M32247; AAA40788.1; -;
 DR EMBL; D00675; BAA00579.1; -;
 DR EMBL; X16273; CAA34349.1; -;
 DR PIR; A33892; ITRT.
 DR HSP; P01009; IOMB.
 DR InterPro; IPR00215; Prot_inh_serpin.
 DR Pfam; PF00079; Serpin; 1.
 DR SMART; SM00093; SERPIN; 1.
 DR PROSITE; PS00284; SERPIN; 1.
 KW Direct protein sequencing; Glycoprotein; Plasma;
 KW Serine protease inhibitor; Serpin; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 411 Alpha-1-antitrypsinase.
 FT SITE 376 377 Reactive bond.
 FT CARBOHYD 64 64 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 101 101 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 265 265 N-linked (GlcNAc. .) (Potential).
 FT CONFLICT 14 14 A -> G (in Ref. 2).
 FT CONFLICT 84 84 L -> V (in Ref. 2).
 FT CONFLICT 247 247 M -> I (in Ref. 3).
 FT CONFLICT 248 248 H -> Y (in Ref. 2).
 FT CONFLICT 318 318 K -> N (in Ref. 2).
 FT CONFLICT 322 322 S -> D (in Ref. 3).
 SQ SEQUENCE 411 AA; 46135 MW; B4245CFE21C5C761 CRC64;

Query Match 71.0%; Score 1443.5; DB 1; Length 411;
 Best Local Similarity 69.9%; Pred. No. 6.1e-88;
 Matches 269; Conservative 62; Mismatches 53; Indels 1; Gaps 1;

QY 8 AQKTDTHDQDHPNTFNKIPNLAFAPSLYROLAQHSNTIFFSPVSTATAFAMLSLG 67
 DB 27 AQETDTSQDQS--PTYRKISSNLADFAFSLYRELHVQSNSTNSIFFSPMSITTAFAMLS 85
 QY 68 TKADTHDEILGLNPNLTQIPRAQIHGSPQELLTLNOPSOLQTLTGNGFLSOGKLV 127
 DB 86 SKGDTKQKLEGLFELNLTQIPDAIHKAFLHLLQTLNRPDSELQTLTGNGFLVKNKLV 145
 QY 128 DKFLDVKLYHSAFTWFGDTEQAOKQINDVVEKGTQKQIVDLVKELDRDTVFALVY 187
 DB 146 EKFLVEVKVNYHSAFVSFVADSEAKKINDVVEKGTQKQIVDLVKELDRDTVFALVY 205
 QY 188 IFPGKWERPFEVKOTBEEDFHVQDVQVTVKVPMMKRLGMFNIQHCCKLSSWVLLMKYLG 247
 DB 206 IFPGKWERPFEVKOTBEEDFHVQDVQVTVKVPMMKRLGMFNIQHCCKLSSWVLLMKYLG 265
 QY 248 ATAIFPLPDGKLOHLENELTHDIITKFLNEDRSASLHLPKLSITGTYDLKSVLGQIG 307
 DB 266 ATAIFLLPDGKLOHLEDDITKFLAKFLKRRSSVNLHFPKLSITGTYDLKSVLTRLG 325
 QY 308 ITKVFSGADLSGVTEAPLKLKSAVHKAVLTIDKGTGAAGAMFLERIPRSPPEVKFN 367
 DB 326 ITRVFNNDADLSGITEDAPLKLKSAVHKAVLTIDERGTEAAGATVVEAVPMSPPEVKFD 385
 QY 368 KPFVFLMIEQNTKSPPLFMGKVNP 392
 DB 386 HPFIFMIVESETQSPPLFVGKVNP 410

RESULT 10

Q6AYZ5 PRELIMINARY; PRT; 411 AA.
 AC Q6AYZ5;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Serine protease inhibitor alpha 1.
 GN Names=Serpinal;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=101116;
 RN [1]
 RP SEQUENCE FROM N.A.


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RN  SEQUENCE FROM N.A.
RP  TISSUE=Liver;
RC  MEDLINE=96004896; PubMed=7548212; DOI=10.1016/0167-4781(95)00140-C;
RA  Nakatani T., Suzuki Y., Yoshida K., Sinohara H.;
RX  "Molecular cloning and sequence analysis of cDNA encoding plasma
RT  alpha-1-antitrypsinase from Syrian hamster: implications for the
RT  evolution of Rodentia.";
RL  Biochem. Biophys. Acta 1263:245-248 (1995).
CC  -1- SIMILARITY: Belongs to the serpin family.
DR  EMBL; D49709; BAA08557.1; -.
DR  PIR; S60036; S60036.
DR  HSSP; P01009; IQMB.
DR  GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR  InterPro; IPR000215; Prot_inh_serpin.
DR  Pfam; PF00079; Serpin; 1.
DR  SMART; SM00093; SERPIN; 1.
KW  Protease inhibitor; Serine protease inhibitor; Serpin; Signal.
FT  SIGNAL 1 24 Potential..
FT  CHAIN 25 413 alpha-1-antitrypsinase.
SQ  SEQUENCE 413 AA; 45819 MW; 71D192E106A1EB36 CRC64;

Query Match 70.4%; Score 1431.5; DB 2; Length 413;
Best Local Similarity 70.2%; Pred. No. 3.9e-87;
Matches 271; Conservative 55; Mismatches 59; Indels 1; Gaps 1;

QY 8 AQKTDTHSHDQDHPFTFNKIPNLAEFAFSLYROLAQHSNSTIFFSPVSIATAFAMLSLG 67
DB 27 AQETDASKQDQEQHQAQCKKIAPNLAEFAFSLYRELHQSNSTIFFSPVSIATAFAMLSLG 86
QY 68 TKADTHDEILLEGFLNLTQIPEAQIHGEGFQELLRTLNQDPSQLQLTGNGFLSQGLKLV 127
DB 87 TKGVTHTQILEGFLNLTAEAEVHKGFHNLQTFNRPDNEQLQTTGNGFLFHNNKLV 146
QY 128 DKFLEDVKKLYHSEAFVFNPGDTEQAQKQINDVVEKGTQKIVDLVKELDRDTPFALVNY 187
DB 147 DKFLEEVKNDYHSEAFVFNPGDTEQAQKQINDVVEKGTQKIVDLVKELDRDTPFALVNY 206
QY 188 IFFPKGWRPFPEVKDTEEDFHVQDQVTVKVPMMKRLGMFNIQHKCKLSWLLMKYLG 247
DB 207 IFFPKGWRPFPEVKDTEEDFHVQDQVTVKVPMMKRLGMFNIQHKCKLSWLLMKYLG 266
QY 248 ATAIFLPEDEKGLQHLNETHDIITKFLNEDRRSASLHLPKLSITGYDLSKVSQGLG 307
DB 267 ATAIFLPEDEKGLQHLNETHDIITKFLNEDRRSASLHLPKLSITGYDLSKVSQGLG 326
QY 308 ITKVFNSGADLSGVTEEAFLKSKAVHKAVLTIDEKGTGAAGAMFLERIPRSTPPVKEN 367
DB 327 ITKVFNSGADLSGVTEEAFLKSKAVHKAVLTIDEKGTGAAGAMFLERIPRSTPPVKEN 386
QY 368 KPFVFLMIEQNT-KSLPFGMKVYNPT 392
DB 387 SPIAIYDRQTAQKSPFLVGVKVDPT 412

RESULT 13
ALAT SHEEP
ID ALAT SHEEP STANDARD; PRT; 416 AA.
AC P12725;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Alpha-1-antitrypsinase precursor (Alpha-1-antitrypsin) (Alpha-1-
DE proteinase inhibitor).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Eutelestomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=89366677; PubMed=2788872;

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RA Brown W.M., Dziegielewska K.D., Foreman R.C., Saunders N.R., Wu Y.;
RT "Nucleotide and deduced amino acid sequence of sheep alpha 1
RT antitrypsin.";
RL Nucleic Acids Res. 17:6398-6398 (1989).
RN [2]
RP SEQUENCE OF 25-55.
RC TISSUE=Plasma;
RX MEDLINE=9114455; PubMed=1899999;
RA Mistry R., Snashall P.D., Totty N., Guz A., Tetley T.D.;
RT "Isolation and characterization of sheep alpha 1-proteinase
RT inhibitor.";
RL Biochem. J. 273:685-690 (1991).
CC -1- FUNCTION: Inhibits human leukocyte elastase, pig pancreatic
CC elastase and bovine trypsin on a 1:1 molar basis.
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: Plasma.
CC -1- SIMILARITY: Belongs to the serpin family.
CC -----
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CC -----
DR EMBL; X15555; CAA33561.1; -.
DR PIR; S05312; ITSH.
DR HSSP; P01009; IQMB.
DR InterPro; IPR000215; Prot_inh_serpin.
DR Pfam; PF00079; Serpin; 1.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; 1.
KW Direct protein sequencing; Glycoprotein; Plasma;
KW Serine protease inhibitor; Serpin; Signal.
FT SIGNAL 1 24
FT CHAIN 25 416 Alpha-1-antitrypsinase.
FT SITE 380 381 Reactive bond.
FT CARBOHYD 68 68 N-linked (GlcNAc.. ) (Potential).
FT CARBOHYD 105 105 N-linked (GlcNAc.. ) (Potential).
FT CARBOHYD 143 143 N-linked (GlcNAc.. ) (Potential).
FT CARBOHYD 269 269 N-linked (GlcNAc.. ) (Potential).
FT CONFLICT 39 39 A -> S (in Ref. 2).
FT CONFLICT 45 45 C -> A (in Ref. 2).
SQ SEQUENCE 416 AA; 45984 MW; 0B4702C0527321BF CRC64;

Query Match 70.4%; Score 1430; DB 1; Length 416;
Best Local Similarity 69.2%; Pred. No. 4.9e-87;
Matches 269; Conservative 62; Mismatches 56; Indels 2; Gaps 1;

QY 4 QGDAAQKTDTSHDQDHPFTFNKIPNLAEFAFSLYROLAQHSNSTIFFSPVSIATAFAM 63
DB 28 QGHAVQETDDTAHQE--AACHKIAPNLAEFAFSLYROLAQHSNSTIFFSPVSIATAFAM 85
QY 64 LSLGKTADTHDEILLEGFLNLTQIPEAQIHGEGFQELLRTLNQDPSQLQLTGNGFLSQGL 123
DB 86 LSLGAKGNTHTEILEGFLNLTAEAEVHKGFHNLQTFNRPDNEQLQTTGNGFLFINS 145
QY 124 LKLVKFLVDKLYHSEAFVFNPGDTEQAQKQINDVVEKGTQKIVDLVKELDRDTPFA 183
DB 146 AKLVDTFLEDVKNLHSHKAFSINFRDAEBAKKKINDVVEKSHGKIVDLVKELDRDTPFA 205
QY 184 LVNYIFFKGRPFPEVKDTEEDFHVQDQVTVKVPMMKRLGMFNIQHKCKLSWLLMK 243
DB 206 LVNYISFKGKWEKPEVEHTERDHFVNEQTVKVPMMKRLGMFNIQHKCKLSWLLMK 265
QY 244 YLGNTAIFLPEDEKGLQHLNETHDIITKFLNEDRRSASLHLPKLSITGYDLSKVS 303
DB 266 YVGNVTACFILPDGLKQLQLEDKLNELAKFLKKYASSANLHLPKLSITGYDLSKVS 325
QY 304 GOLGITKVFNSGADLSGVTEEAFLKSKAVHKAVLTIDEKGTGAAGAMFLERIPRSTPP 363
DB 326 GELGINRVFNSGADLSGVTEEAFLKSKAVHKAVLTIDEKGTGAAGAMFLERIPRSTPP 385

```


Qy	308	ITKVFSNGADLSGVTEEAPLKLKAVHKAVLTIDEKGTAAAGAMFLERIPRSIPPEVKFN	367
Db	327	ITKVFSQADLSGVTEEAPLTVSKGLHKAVLDIHEKGTDAAGATFLEMIPMLPSDLKFD	386
Qy	368	KPFVFLMIEONTKSPFLFMGKVNPT	392
Db	387	RPFLVVIYEHHTKSPLFVGVKNPT	411

Search completed: June 20, 2005, 19:45:54
Job time : 175 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2005, 19:34:19 ; Search time 75 Seconds
(without alignments)
2031.781 Million cell updates/sec

Title: PDX1
Perfect score: 2032
Sequence: 1 EDPOGDAQAQTUHTSHDQD.....IEQNTKSLFMGKVVNPTGK 394

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : A_Geneseq_16Dec04:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2032	100.0	394	2	AAY44201
2	2026	99.7	394	2	AAY44205
3	2003	98.6	394	2	AAY59839
4	2003	98.6	394	5	AAY99873
5	2003	98.6	398	8	ADM82878
6	2003	98.6	418	1	AAP40133
7	2003	98.6	418	1	AAP94664
8	2003	98.6	418	2	AAY26925
9	2003	98.6	418	5	ABG96414
10	2003	98.6	418	6	ABR55849
11	2003	98.6	418	7	ADB99858
12	2003	98.6	418	7	ADG63536
13	2003	98.6	418	7	ADG63532
14	2003	98.6	418	7	ADG63524
15	2003	98.6	418	7	ADG28921
16	2003	98.6	418	7	ADG25246
17	2003	98.6	418	8	ADG25246
18	2003	98.6	418	8	ADNA9694
19	2003	98.6	418	8	ADM82877
20	2003	98.6	503	5	AAY99884
21	2003	98.6	503	5	AAY99881
22	2003	98.6	522	5	AAY99883
23	2003	98.6	522	5	AAY99885
24	2003	98.6	580	5	AAY99882
25	2003	98.6	580	5	AAY99889

99 1311 64.5 418 7 ADE08102 Novel pro
100 1301 64.0 413 2 AAW23649 Recombina

ALIGNMENTS

```

RESULT 1
AA44201
ID AAY44201 standard; protein; 394 AA.
AC AAY44201;
DT 25-JAN-2000 (first entry)
DE Alpha-1 antitrypsin variant Portland.
KW Alpha-1 antitrypsin variant Portland; alpha-1 antitrypsin; PDX;
KW protease inhibitor; furin endoprotease; peptide mimetic; bacterial toxin;
KW furin recognition site; portland protein; SYBYL program; pharmacophore;
KW protein crystal structure analysis; reactive site loop; RSL;
KW endolytic maturation; endoproteolytic activation; Pseudomonas aeruginosa;
KW Corynebacterium diptheriae; Bacillus anthracis; cytomegalovirus;
KW biologically active protein.
OS Synthetic.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Misc-difference 355 /note= "Wild type Ala substituted by Arg"
FT Misc-difference 358 /note= "Wild type Met substituted by Arg"
FT
FT
FT
PN WO9951624-A1.
XX
XX 14-OCT-1999.
XX
XX 08-APR-1999; 99WO-US007776.
XX
XX 08-APR-1998; 98US-0081034P.
XX
XX (UYOR-) UNIV OREGON HEALTH SCI.
XX
XX Jean F, Thomas G;
XX
XX WPI; 1999-620190/53.
XX
XX New furin endoprotease inhibitor that mimics a specific region of alpha-1
XX antitrypsin Portland mutant, for treatment and prevention of bacterial
XX and viral infection.
XX
XX Claim 1; Page 98-99; 108pp; English.
XX
XX The present sequence is alpha-1 antitrypsin mutated variant Portland
XX (also termed PDX). This effectively inhibits furin endoprotease. Peptides
XX or peptide mimetics derived from this sequence inhibit bacterial toxins
XX that are processed at a consensus furin recognition site, when
XX administered in therapeutically effective amounts. Portland protein
XX generated by the SYBYL program and the crystal structure analysed for
XX designing the pharmacophore for the reactive site loop of the Portland
XX variant. Endoproteolytic activation of bacterial toxins and endolytic
XX maturation of viral proteins is blocked by the peptide and peptide
XX mimetics. This is useful in treating infections of cells by bacteria
XX (specifically Corynebacterium diptheriae, Bacillus anthracis and
XX Pseudomonas aeruginosa) or viruses (specifically cytomegalovirus). It may
XX also be used to inhibit processing of biologically active proteins
XX
XX Sequence 394 AA;

```

Query Match 100.0%; Score 2032; DB 2; Length 394;
Best Local Similarity 100.0%; Pred. No. 5.5e-158;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDPOGDAAKTDTSHDDHPTFNKITPNLAEFAFSLYRQLAHQSNSTNIFSPVSIATA 60
DB 1 EDPOGDAAKTDTSHDDHPTFNKITPNLAEFAFSLYRQLAHQSNSTNIFSPVSIATA 60
QY 61 FAMLISLGTAKADTHDEILGLNPNLTQIPEAQIHGFGQBELRLTNQPSQLQTTGNGLFL 120
DB 61 FAMLISLGTAKADTHDEILGLNPNLTQIPEAQIHGFGQBELRLTNQPSQLQTTGNGLFL 120
QY 121 SQGLKLVDFKEDVKLYHSEAFVNFQGTQOAKKOINDYVEKGTQGIKIVDLVKELDRDT 180
DB 121 SQGLKLVDFKEDVKLYHSEAFVNFQGTQOAKKOINDYVEKGTQGIKIVDLVKELDRDT 180
QY 181 VVALVNYIFFFGKWERPPEVKDTEEDFHVDQVTVKVPMMKRLGMFNIQHCKLSSWVL 240
DB 181 VVALVNYIFFFGKWERPPEVKDTEEDFHVDQVTVKVPMMKRLGMFNIQHCKLSSWVL 240
QY 241 LMKYLGNAITAFPLPDEGKLOHLENELTHDITKPLENEDRRRSASLHLPKLSITGTYDLK 300
DB 241 LMKYLGNAITAFPLPDEGKLOHLENELTHDITKPLENEDRRRSASLHLPKLSITGTYDLK 300
QY 301 SVLGGLGITKTVFSGADLSGVTEERAPLKLKAVHKAVLTIDEKGTAAAGMFLERIPRSI 360
DB 301 SVLGGLGITKTVFSGADLSGVTEERAPLKLKAVHKAVLTIDEKGTAAAGMFLERIPRSI 360
QY 361 PPEVKFNKPFVFLMIEQNTKSPLEFMGKVVNPTGK 394
DB 361 PPEVKFNKPFVFLMIEQNTKSPLEFMGKVVNPTGK 394

RESULT 2

AA44205
ID AAY44205 standard; protein; 394 AA.

AC AAY44205;

DT 25-JAN-2000 (first entry)

DE Alpha-1 antitrypsin variant Pittsburgh.

XX Alpha-1 antitrypsin variant Pittsburgh; alpha-1 antitrypsin; PIT;
KW negative control; furin inhibition assay; peptide mimetic; A7 cell;
KW Pseudomonas aeruginosa exotoxin A; PEA; HCMV glycoprotein gB.
XX
XX Synthetic.
XX Homo sapiens.

OS

XX

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CC inhibition assay to assess the biological activity of the peptide
 CC mimetics. A7 cells when incubated with PIR exhibited little or no
 CC protective effect in the presence of Pseudomonas aeruginosa exotoxin A.
 CC PIR was also used as a negative control for the assay to detect PDX -
 CC mediated inhibition of furin-catalysed maturation of HCMV glycoprotein gB
 XX
 XX Sequence 394 AA;

Query Match 99.7%; Score 2026; DB 2; Length 394;
 Best Local Similarity 99.7%; Pred. No. 1.7e-157;
 Matches 393; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDPOGDAQAQKTDTSHHDDQDHPFNKIPNLAFAFSLYRQLAHQSNSTNIPFSPVSIATA 60
 DB 1 EDPOGDAQAQKTDTSHHDDQDHPFNKIPNLAFAFSLYRQLAHQSNSTNIPFSPVSIATA 60
 QY 61 FAMLISLGTAKDTHDEILEGLNFNLTQIPQAQIHGEGFQELLRTLNQDPSQLQTTGNGLFL 120
 DB 61 FAMLISLGTAKDTHDEILEGLNFNLTQIPQAQIHGEGFQELLRTLNQDPSQLQTTGNGLFL 120
 QY 121 SQGLKLVDFLEVDVKLYHSEAFVNFVFGDTEQAQKQINDYVEKGTQGIKIVDLVKELDRDT 180
 DB 121 SQGLKLVDFLEVDVKLYHSEAFVNFVFGDTEQAQKQINDYVEKGTQGIKIVDLVKELDRDT 180
 QY 181 VFALVNYIFFKQKWERPFVVKDTEEDFHVQDVTTVKVPMMKRLGMFNHCHCKLSSWYL 240
 DB 181 VFALVNYIFFKQKWERPFVVKDTEEDFHVQDVTTVKVPMMKRLGMFNHCHCKLSSWYL 240
 QY 241 LMKYLGNAATAIFFLPDEGKLOHLENELTHDIITKFLNEDRRSASLHLPKLSITGYDIJK 300
 DB 241 LMKYLGNAATAIFFLPDEGKLOHLENELTHDIITKFLNEDRRSASLHLPKLSITGYDIJK 300
 QY 301 SVLGQGITKVFSGADLSGVTEEAAPLKLKSAVKAVLTIDEKGTAAAGAMFLERIPRSI 360
 DB 301 SVLGQGITKVFSGADLSGVTEEAAPLKLKSAVKAVLTIDEKGTAAAGAMFLERIPRSI 360
 QY 361 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPTGK 394
 DB 361 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPTGK 394

RESULT 3

AAW59839
 ID AAW59839 standard; protein; 394 AA.
 XX
 AC AAW59839;
 XX
 DT 20-NOV-1998 (first entry)
 XX
 DE Mature protein sequence of alpha1-antitrypsin (AAT).
 XX
 KW Protein expression; monocotyledon plant cell;
 KW glycosylated alpha 1-antitrypsin; AAT; glycosylated antithrombin III;
 KW Atrial; human serum albumin; HSA; subtilisin BPN'; treatment; emphysema;
 KW antithrombotic; blood replacement.

XX Homo sapiens.
 XX
 XX WO9836085-A1.
 XX
 PD 20-AUG-1998.
 XX
 PF 13-FEB-1998; 98WO-US003068.
 XX
 PR 13-FEB-1997; 97US-0037991P.
 PR 13-FEB-1997; 97US-0038168P.
 PR 13-FEB-1997; 97US-0038169P.
 PR 13-FEB-1997; 97US-0038170P.
 XX
 PA (PHYT-) APPLIED PHYTOLOGICS INC.
 XX
 XX Sutliff TD, Rodriguez RL;
 XX

WPI; 1998-467179/40.
 N-PSDB; AAV411726.

Expressing mature, glycosylated proteins in monocotyledonous plant cells
 - from chimeric gene including signal peptide sequence, specifically
 therapeutic agents and industrial enzymes.

Disclosure; Page 28-29; 53pp; English.

The present sequence represents the mature protein of alpha1-antitrypsin (AAT). The protein is used to exemplify the invention. The specification describes a method for producing mature heterologous protein in monocotyledonous plant cells. The method comprises transforming the cells with a chimeric gene comprising a monocotyledonous transcription regulator, inducible either during seed maturation or by adding/removing a small molecule, DNA encoding the heterologous protein, and DNA encoding a signal peptide, with the signal peptide causing secretion of the protein from the cell. Proteins expressed in this manner include mature glycosylated alpha 1-antitrypsin (AAT) with a glycosylation pattern that significantly increases its serum half-life, mature glycosylated antithrombin III (Atrial), mature human serum albumin (HSA) having the native folding pattern as shown by bilirubin-binding characteristics, or mature active subtilisin BPN'. These proteins are useful therapeutically (e.g. AAT for treating emphysema, Atrial as antithrombotic and HSA as blood replacement) or as industrial enzymes (BPN' is used in detergents)

Sequence 394 AA;

Query Match 98.6%; Score 2003; DB 2; Length 394;
 Best Local Similarity 98.5%; Pred. No. 1.3e-155;
 Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDPOGDAQAQKTDTSHHDDQDHPFNKIPNLAFAFSLYRQLAHQSNSTNIPFSPVSIATA 60
 DB 1 EDPOGDAQAQKTDTSHHDDQDHPFNKIPNLAFAFSLYRQLAHQSNSTNIPFSPVSIATA 60
 QY 61 FAMLISLGTAKDTHDEILEGLNFNLTQIPQAQIHGEGFQELLRTLNQDPSQLQTTGNGLFL 120
 DB 61 FAMLISLGTAKDTHDEILEGLNFNLTQIPQAQIHGEGFQELLRTLNQDPSQLQTTGNGLFL 120
 QY 121 SQGLKLVDFLEVDVKLYHSEAFVNFVFGDTEQAQKQINDYVEKGTQGIKIVDLVKELDRDT 180
 DB 121 SQGLKLVDFLEVDVKLYHSEAFVNFVFGDTEQAQKQINDYVEKGTQGIKIVDLVKELDRDT 180
 QY 181 VFALVNYIFFKQKWERPFVVKDTEEDFHVQDVTTVKVPMMKRLGMFNHCHCKLSSWYL 240
 DB 181 VFALVNYIFFKQKWERPFVVKDTEEDFHVQDVTTVKVPMMKRLGMFNHCHCKLSSWYL 240
 QY 241 LMKYLGNAATAIFFLPDEGKLOHLENELTHDIITKFLNEDRRSASLHLPKLSITGYDIJK 300
 DB 241 LMKYLGNAATAIFFLPDEGKLOHLENELTHDIITKFLNEDRRSASLHLPKLSITGYDIJK 300
 QY 301 SVLGQGITKVFSGADLSGVTEEAAPLKLKSAVKAVLTIDEKGTAAAGAMFLERIPRSI 360
 DB 301 SVLGQGITKVFSGADLSGVTEEAAPLKLKSAVKAVLTIDEKGTAAAGAMFLERIPRSI 360
 QY 361 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPTGK 394
 DB 361 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPTGK 394

RESULT 4

AAU99873
 ID AAU99873 standard; protein; 394 AA.
 XX
 AC AAU99873;
 XX
 DT 07-OCT-2002 (first entry)
 XX
 DE Human alpha-1-antitrypsin (AAT) protein.

XX Alpha-1-antitrypsin; AAT; human; protease inhibitor; malaria; emphysema;
 KW asthma; chronic obstructive pulmonary disease; eczema; cystic fibrosis;

KW otitis media; otitis external; HIV; psoriasis;
KW human immunodeficiency virus; atopic dermatitis; muscular dystrophy;
KW herpes; ulceration; sepsis; rheumatoid arthritis; periodontal disease;
KW tumour metastasis; tumour angiogenesis; osteoporosis; Paget's disease;
KW glomerulonephritis; scleroderma; Alzheimer's disease; hypertension.
XX
OS Homo sapiens.
XX
XX WO200250287-A2.
XX
XX 27-JUN-2002.
XX
XX 18-DEC-2001; 2001WO-US049256.
XX
XX 18-DEC-2000; 2000US-0256699P.
XX
XX 20-NOV-2001; 2001US-0331966P.
XX
XX (ARRI-) ARRIVA PHARM INC.
XX
XX Barr PJ, Gibson HL, Pemberton P;
XX
XX WPI; 2002-500631/53.
XX
XX N-PSDB; ABK8015.
XX
XX Novel fusion protein useful for inhibiting protease activity associated
XX with a disorder such as emphysema, asthma, comprises a first protease
XX inhibitor comprising alpha 1-antitrypsin and a second protease inhibitor.
XX
XX Claim 25; Page 25-27; 134pp; English.
XX
XX This invention relates to a novel fusion protein comprising a first
XX protease inhibitor comprising an alpha1-antitrypsin or its functionally
XX active portion and a second protease inhibitor or its functionally active
XX protein. The fusion proteins of the invention may act as an inhibitor of
XX protease activity. The fusion protein of the invention is useful for
XX inhibiting protease activity associated with a disorder such as
XX emphysema, asthma, chronic obstructive pulmonary disease, cystic
XX fibrosis, otitis media, otitis external or HIV infection, or for treating
XX an individual suffering from or at risk for a disease or disorder
XX involving unwanted protease activity. The proteins are useful for
XX treating dermatological diseases such as atopic dermatitis, eczema and
XX psoriasis, in inflammatory responses to viral infection, and for treating
XX herpes infection, corneal or epidermal ulceration, chronic non-healing
XX wounds, sepsis, rheumatoid arthritis, periodontal disease, tumour
XX metastasis and tumour angiogenesis, gastric ulceration, osteoporosis,
XX Paget's disease, glomerulonephritis, scleroderma, malaria, bacterial
XX infection, Alzheimer's disease, hypertension and muscular dystrophy. The
XX present sequence represents the human alpha-1-antitrypsin (AAT) protein
XX used to create the fusion protein of the invention
XX
XX Sequence 394 AA;
XX
XX Query Match 98.6%; Score 2003; DB 5; Length 394;
XX Best Local Similarity 98.5%; Pred. No. 1.3e-155;
XX Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
XX
XX 1 EDPOGDAQKTTSHHDDPHFNKITNLAEFAFLYRQLAHQSNSTNIFPSPVSIATA 60
XX
XX 1 EDPOGDAQKTTSHHDDPHFNKITNLAEFAFLYRQLAHQSNSTNIFPSPVSIATA 60
XX
XX 61 FAMLISGTKADTHDEILEGLNENLTIQIPRAQIHEGFQELLRTLNQDLSQQLTTCGGLFL 120
XX
XX 61 FAMLISGTKADTHDEILEGLNENLTIQIPRAQIHEGFQELLRTLNQDLSQQLTTCGGLFL 120
XX
XX 121 SGGLKLVKFLVDVKKLVHSEAFVNFNGTEQAQKQINDYVEKGTQGGKIVDLVKELDRPT 180
XX
XX 121 SGGLKLVKFLVDVKKLVHSEAFVNFNGTEQAQKQINDYVEKGTQGGKIVDLVKELDRPT 180
XX
XX 181 VPALVNYLFFKCKRPERPEVKDTEEDHFVDQVTVTKVPMKRLGWNFIQHCKLSSWVL 240
XX
XX 181 VPALVNYLFFKCKRPERPEVKDTEEDHFVDQVTVTKVPMKRLGWNFIQHCKLSSWVL 240
XX
XX 241 LMKYLGNTAIFFLPDEGKQLHLENELTHDIIITKFLNEDRRSASLHLPKLSITGYDLK 300

Db 241 LMKYLGNTAIFFLPDEGKQLHLENELTHDIIITKFLNEDRRSASLHLPKLSITGYDLK 300
Qy 301 SVLGQLGITKTVFSNGADLSGVTTEAPLKLKAVHKAVLTIDEKGTAAAGAMFLERIPRSI 360
Db 301 SVLGQLGITKTVFSNGADLSGVTTEAPLKLKAVHKAVLTIDEKGTAAAGAMFLERIPRSI 360
Qy 361 PPEVKFNKPFVFLMIEQNTKSPFLPMGKVVNPTGK 394
Db 361 PPEVKFNKPFVFLMIEQNTKSPFLPMGKVVNPTGK 394
XX
XX RESULT 5
XX ADM82878
XX ID ADM82878 standard; protein; 398 AA.
XX
XX AC ADM82878;
XX
XX DT 29-JUL-2004 (first entry)
XX
XX DE Mouse alpha-1-antitrypsin (AAT) mature protein SEQ ID NO:4.
XX
XX KW alpha 1-antichymotrypsin; ACT; alpha 1-antitrypsin; AAT; gene therapy;
XX protein therapy; diabetic ulcer; arterial ulcer; ulcus cruris arteriosum;
XX KW necrobiosis lipoidica; ulcera arteriosa; wound healing; human.
XX
XX OS Homo sapiens.
XX
XX FN EP1415664-A1.
XX
XX PD 06-MAY-2004.
XX
XX PF 30-OCT-2002; 2002EP-00024200.
XX
XX PR 30-OCT-2002; 2002EP-00024200.
XX
XX PA (SWIT-) SWITCH BIOTECH AG.
XX
XX PI Halle J, Goppelt A;
XX
XX DR WPI; 2004-341870/32.
XX
XX DR N-PSDB; ADM82879.
XX
XX PT Use of alpha 1-antichymotrypsin polypeptide in combination with alpha 1-
XX antitrypsin polypeptide for treating and/or preventing poorly healing
XX PT diabetes-associated and/or poorly healing arterial wounds e.g., diabetic
XX PT ulcer.
XX
XX PS Claim 2; SEQ ID NO 4; 31pp; English.
XX
XX The present invention describes a method of using alpha 1-
XX antichymotrypsin (ACT), its functional variant and/or encoding nucleic
XX acid, or of a cell expressing ACT polypeptide or its encoding nucleic
XX acid, in combination with alpha 1-antitrypsin (AAT), its functional
XX variant or encoding nucleic acid, or with a cell expressing AAT
XX polypeptide or its encoding nucleic acid, for treating and/or preventing
XX poorly healing diabetes-associated and/or arterial wounds. Also described
XX is a method of manufacturing a pharmaceutical composition for treating
XX and/or preventing the diseases, where the ACT polypeptide or its encoding
XX nucleic acid or a cell expressing the ACT polypeptide or its encoding
XX nucleic acid is combined with the AAT polypeptide or its encoding nucleic
XX acid or a cell expressing the AAT polypeptide or its encoding nucleic
XX acid. ACT and AAT can be used in gene and protein therapy. The ACT and
XX AAT polypeptides (in combination) are useful for treating and/or
XX preventing poorly healing diabetes-associated and/or poorly healing
XX arterial wounds such as diabetic ulcer and arterial ulcer, preferably
XX diabetic ulcer. Diabetic ulcers are skin lesions in mammals and humans
XX suffering from diabetes (e.g., include ulcus cruris arteriosum,
XX necrobiosis lipoidica and ulcera arteriosa) and delayed wound healing is
XX caused by arteriosclerotic destruction of the blood vessels. The present
XX sequence represents the mature human AAT, which is used in the
XX exemplification of the present invention.
XX

SQ Sequence 398 AA;

Query Match 98.6%; Score 2003; DB 8; Length 398;
Best Local Similarity 98.5%; Pred. No. 1.3e-155;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDPOGDAQAQKTTSHHDQDHPFNKITPNLAFAPSLYRQLAHQSNSTNIFPSPVSIATA 60
DB 5 EDPOGDAQAQKTTSHHDQDHPFNKITPNLAFAPSLYRQLAHQSNSTNIFPSPVSIATA 64
QY 61 FAMLISGKTKADTHDEILEGNLNFNLTOIPEAQIHEGFQELLRTLNQDPSQLQTTGNGLFL 120
DB 65 FAMLISGKTKADTHDEILEGNLNFNLTOIPEAQIHEGFQELLRTLNQDPSQLQTTGNGLFL 124
QY 121 SOGLKLVDFKLEDDVKKLYHSEAFNFTVNFQDTEQAQKQINDYVEKGTQGIKIVDLVKELDRDT 180
DB 125 SEGLKLVDFKLEDDVKKLYHSEAFNFTVNFQDTEQAQKQINDYVEKGTQGIKIVDLVKELDRDT 184
QY 181 VFALVNYIIFPKGKWERPPEVKDTEEDFHVDQVTTVKVPMKRLGFMFNIOHCKKLSWWL 240
DB 185 VFALVNYIIFPKGKWERPPEVKDTEEDFHVDQVTTVKVPMKRLGFMFNIOHCKKLSWWL 244
QY 241 LMKYLGNAITAIFFLPDEGKLOHLENELTHDIITKPLENEDRRSASLHLPKLSITGYDILK 300
DB 245 LMKYLGNAITAIFFLPDEGKLOHLENELTHDIITKPLENEDRRSASLHLPKLSITGYDILK 304
QY 301 SVLGQGITKVFNSGADLSGVTEEAPLKLKSAVHKAVLTIDKGTAAAGAMFLERIPRSI 360
DB 305 SVLGQGITKVFNSGADLSGVTEEAPLKLKSAVHKAVLTIDKGTAAAGAMFLERIPRSI 364
QY 361 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPTQK 394
DB 365 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPTQK 398

RESULT 6
AAP40133
ID AAP40133 standard; protein; 418 AA.
AC AAP40133;
DT 25-MAR-2003 (revised)
DT 16-FEB-1992 (first entry)
XX Sequence of human alpha-1-antitrypsin.
DE Protease inhibitor; enzyme; proteolysis inhibitor; emphysema; therapy.
KW Homo sapiens.
OS
FH Key Location/Qualifiers
FT Peptide 1..24
FT /label= signal
FT Region 25..418
XX
PN EP103409-A.
XX
XX 21-MAR-1984.
XX
XX 12-AUG-1983; 83EP-00304668.
XX
XX 13-AUG-1982; 82US-00408099.
PR 13-AUG-1982; 88EP-00201179.
PR 18-AUG-1982; 82US-00409183.
PR 28-APR-1983; 83US-00489406.
XX
XX (ZYMO-) ZYMOS CORP.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
PA (KAWA/) KAWASAKI G H.
XX
XX Kawasaki GH, Woodbury RG;
XX
XX WPI; 1984-077108/13.

DR N-PSDB; AAM40078.
XX
XX Extra:chromosomal element for replication in yeast - with yeast promoter
PT for regulation of glycolytic protein prodn.
XX
XX Disclosure; Fig 1A; 48pp; English.
XX
XX The inventors claim a DNA construct contg. a gene encoding human alpha-1-
CC antitrypsin. A substantially pure, substantially unglycosylated mammalian
CC alpha-1-antitrypsin is also claimed. (Updated on 25-MAR-2003 to correct
CC PA field.)
XX
SQ Sequence 418 AA;

Query Match 98.6%; Score 2003; DB 1; Length 418;
Best Local Similarity 98.5%; Pred. No. 1.4e-155;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDPOGDAQAQKTTSHHDQDHPFNKITPNLAFAPSLYRQLAHQSNSTNIFPSPVSIATA 60
DB 25 EDPOGDAQAQKTTSHHDQDHPFNKITPNLAFAPSLYRQLAHQSNSTNIFPSPVSIATA 84
QY 61 FAMLISGKTKADTHDEILEGNLNFNLTOIPEAQIHEGFQELLRTLNQDPSQLQTTGNGLFL 120
DB 85 FAMLISGKTKADTHDEILEGNLNFNLTOIPEAQIHEGFQELLRTLNQDPSQLQTTGNGLFL 144
QY 121 SOGLKLVDFKLEDDVKKLYHSEAFNFTVNFQDTEQAQKQINDYVEKGTQGIKIVDLVKELDRDT 180
DB 145 SEGLKLVDFKLEDDVKKLYHSEAFNFTVNFQDTEQAQKQINDYVEKGTQGIKIVDLVKELDRDT 204
QY 181 VFALVNYIIFPKGKWERPPEVKDTEEDFHVDQVTTVKVPMKRLGFMFNIOHCKKLSWWL 240
DB 205 VFALVNYIIFPKGKWERPPEVKDTEEDFHVDQVTTVKVPMKRLGFMFNIOHCKKLSWWL 264
QY 241 LMKYLGNAITAIFFLPDEGKLOHLENELTHDIITKPLENEDRRSASLHLPKLSITGYDILK 300
DB 265 LMKYLGNAITAIFFLPDEGKLOHLENELTHDIITKPLENEDRRSASLHLPKLSITGYDILK 324
QY 301 SVLGQGITKVFNSGADLSGVTEEAPLKLKSAVHKAVLTIDKGTAAAGAMFLERIPRSI 360
DB 325 SVLGQGITKVFNSGADLSGVTEEAPLKLKSAVHKAVLTIDKGTAAAGAMFLERIPRSI 384
QY 361 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPTQK 394
DB 385 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPTQK 418

RESULT 7
AAP94664
ID AAP94664 standard; protein; 418 AA.
AC AAP94664;
DT 25-MAR-2003 (revised)
DT 28-JUN-1990 (first entry)
XX
XX Predominant form of human alpha-1-antitrypsin as encoded by cDNA.
KW Human alpha-1-tryptase (hAT); anti-AT antibodies; proteolytic activity;
KW AT deficiency; Saccharomyces cerevisiae GK100; 2-mu plasmid DNA; CATI;
KW Plasmid HAT4; yeast TPI promoter; yeast TPI terminator; plasmid Cl/L.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Peptide 1..118
FT Protein 119..418
XX
XX EP304971-A.
XX
XX 01-MAR-1989.
XX
XX 12-AUG-1983; 88EP-00201179.
PF

```
XX 13-AUG-1982;      82US-00408099.
PR 28-APR-1983;      83US-00489406.
XX (ZYMO ) ZYMOGENETICS INC.
XX Kawasaki GH, Woodbury RG;
XX WPI: 1989-062651/09.
DR N-PSDB; AAN91077.
XX New alpha-1-antitrypsin polypeptide(s) - produced by recombinant DNA
PT techniques, esp. using yeast host.
PT Disclosure; Page ?; 28pp; English.
XX
XX New in the patent are unglycosylated polypeptides having the amino acid
CC sequence of a mammalian alpha-1-antitrypsin (AT). Also claimed is the
CC prodn. of polypeptides having the protease-inhibiting activity of a
CC mammalian AT. A culture of microorganisms is grown such as fungi or
CC yeast, esp. Saccharomyces cerevisiae GK 100, which are transformed with a
CC DNA transfer vector 2-mu plasmid, plasmid CAT1 or plasmid HAT4, contg. a
CC segment encoding the mammalian AT. The unglycosylated polypeptides are
CC useful for prodn. of anti-AT antibodies, for modulating proteolytic
CC activity in mammals, and for treating AT deficiency, esp. for replacing
CC AT which has been inactivated (oxidised) by tobacco or other smoke. In
CC the given example plasmid HAT4 comprises the yeast promoter, an
CC ATGAGGATCC adapter, the HAT gene and the yeast TPI terminator inserted
CC into plasmid CI/1, which contains the entire 2-mu DNA from S. cerevisiae.
CC S. cerevisiae GK100 transformed with HAT4 produces soluble protein with
CC an HAT content of 2-3% when grown on a medium contg. 6% glucose. (Updated
CC on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
CC PR field.)
XX
SQ Sequence 418 AA;
Query Match      98.6%; Score 2003; DB 1; Length 418;
Best Local Similarity 98.5%; Pred. No. 1.4e-155;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 EDPQGDAAQKTDTSHHDQDHPFNKITPNLAEFAFSLYRQLAHQSNSTNIFPSPVSIATA 60
DB 25 EDPQGDAAQKTDTSHHDQDHPFNKITPNLAEFAFSLYRQLAHQSNSTNIFPSPVSIATA 84
QY 61 FAMLISGTKADTHDETLLEGNLNLTQIPEAQIHGFGQELLRTLNQDPSQLQTTGNGLFL 120
DB 85 FAMLISGTKADTHDETLLEGNLNLTQIPEAQIHGFGQELLRTLNQDPSQLQTTGNGLFL 144
QY 121 SGLKLVDKFLDVKKLYHSEAFVNFQDTEQAKQINDYVEKGQKIVDVLVKELDRDT 180
DB 145 SGLKLVDKFLDVKKLYHSEAFVNFQDTEQAKQINDYVEKGQKIVDVLVKELDRDT 204
QY 181 VFALVNYIFFKGKWERPFVKDTEBEDFHDVQVTVTKVPMKRLGMFNIOHCKLSSWVL 240
DB 205 VFALVNYIFFKGKWERPFVKDTEBEDFHDVQVTVTKVPMKRLGMFNIOHCKLSSWVL 264
QY 241 LMKYLGNAITAFELPDDEGKLQHLNELTHDITTKFLENEDRSASLHLPKLSITGYDLK 300
DB 265 LMKYLGNAITAFELPDDEGKLQHLNELTHDITTKFLENEDRSASLHLPKLSITGYDLK 324
QY 301 SVLGQLGITKVFNSGADLSGVTEEAPLKLKAVHKAVLTIDKGTAAAGAMFLERIPRSI 360
DB 325 SVLGQLGITKVFNSGADLSGVTEEAPLKLKAVHKAVLTIDKGTAAAGAMFLERIPMSI 384
QY 361 PPEVFNKPFVFLMIEQNTKSPFLFMGKVVNPTGK 394
DB 385 PPEVFNKPFVFLMIEQNTKSPFLFMGKVVNPTQK 418
```

RESULT 8

AAY26925

ID AAY26925 standard; protein; 418 AA.

XX

```
AC AAY26925;
XX 21-DEC-1999 (first entry)
XX Human alpha1-anti-trypsin type M1 protein.
XX Human; alpha-1-anti-trypsin; transgenic plant; monocotyledon; variant;
KW glycosylation; serine protease; inhibitor; neutrophil; elastase; trypsin;
KW cathepsin G; thrombin; pulmonary tissue; protease damage; septic shock;
KW pulmonary emphysema; cystic fibrosis; rheumatism; recombinant;
KW virus contamination; immunogenicity; ss.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FT Peptide 1..24
FT Protein /label= signal_peptide
FT /label= mature protein
FT Modified-site 70
FT /note= "putative glycosylation site"
FT Modified-site 107
FT Modified-site 271
FT Active-site 382..387
FT /note= "putative active site"
XX WO938987-A1.
XX 05-AUG-1999.
XX 29-JAN-1999; 99WO-FR000195.
XX 30-JAN-1998; 98FR-00001089.
XX (MERI-) MERISTEM THERAPEUTICS.
XX Gruber V, Olagnier B, Bournat P, Theisen M, Merot B;
XX WPI: 1999-469334/39.
XX N-PSDB; AAX83548.
XX Production of alphas-1-antitrypsin, and its variants, in cells of
PT monocotyledonous plants, useful as serine protease inhibitors for
PT therapy, e.g. of emphysema, in cosmetics and as reagents.
XX Claim 8; Fig 1; 67pp; French.
XX This sequence represents the coding region of the human alpha-1-anti-
CC trypsin (AT) gene. The invention relates to the production of AT in plant
CC cells, especially monocotyledonous plants. Also produced are variants of
CC the AT protein, in which the glycosylation pattern of the protein is
CC altered. AT inhibits serine proteases, specifically neutrophil elastase
CC (but also trypsin, cathepsin G, thrombin etc.) so protect pulmonary
CC tissue against protease damage. AT are used to treat AT-deficiency
CC conditions, particularly pulmonary emphysema, cystic fibrosis, septic
CC shock and rheumatism. The use of plants for the recombinant production of
CC AT results in a product without risk of (sub)viral contamination. The
CC recombinant AT had good activity and is stable, with low immunogenicity
CC (associated with glycosylation patterns similar to the native protein)
XX
SQ Sequence 418 AA;
Query Match      98.6%; Score 2003; DB 2; Length 418;
Best Local Similarity 98.5%; Pred. No. 1.4e-155;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 EDPQGDAAQKTDTSHHDQDHPFNKITPNLAEFAFSLYRQLAHQSNSTNIFPSPVSIATA 60
DB 25 EDPQGDAAQKTDTSHHDQDHPFNKITPNLAEFAFSLYRQLAHQSNSTNIFPSPVSIATA 84
QY 61 FAMLISGTKADTHDETLLEGNLNLTQIPEAQIHGFGQELLRTLNQDPSQLQTTGNGLFL 120
DB 85 FAMLISGTKADTHDETLLEGNLNLTQIPEAQIHGFGQELLRTLNQDPSQLQTTGNGLFL 144
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QY 1 EDPOGDAQAQKTDTSHHDDQDPTFNKIPNLAEFAFSLYRQLAHQSNSTNIFPSPVSIATA 60
 DB 25 EDPOGDAQAQKTDTSHHDDQDPTFNKIPNLAEFAFSLYRQLAHQSNSTNIFPSPVSIATA 84
 QY 61 FAMLISLGTAKADTHDEILEGLNPNLTQIPRAQIHGEGFQELLRTLNQDPSQLQTLTNGGLFL 120
 DB 85 FAMLISLGTAKADTHDEILEGLNPNLTQIPRAQIHGEGFQELLRTLNQDPSQLQTLTNGGLFL 144
 QY 121 SQGLKLVDPLEVDVKKLYHSEAFVNFVFGDTEQAQKQINDYVEKGTQGIKIVDLVKELDRDT 180
 DB 145 SEGKLVDPLEVDVKKLYHSEAFVNFVFGDTEQAQKQINDYVEKGTQGIKIVDLVKELDRDT 204
 QY 181 VPALVNYIYFFKQWEPFVKDTEEDFHVDQVTVTKVPMKRLGFMFNTOHCKKLSWWL 240
 DB 205 VPALVNYIYFFKQWEPFVKDTEEDFHVDQVTVTKVPMKRLGFMFNTOHCKKLSWWL 264
 QY 241 LMKYLGNAITAIFFLPDEGKLOHLENLTHDITTKFLENEDRRSASLHLPKLSITGYDLK 300
 DB 265 LMKYLGNAITAIFFLPDEGKLOHLENLTHDITTKFLENEDRRSASLHLPKLSITGYDLK 324
 QY 301 SVLGQIGITKVFNSGADLSGVTEEAFLKLSKAVHKAVALTIDEKGTAAAGAMFLERIPRSI 360
 DB 325 SVLGQIGITKVFNSGADLSGVTEEAFLKLSKAVHKAVALTIDEKGTAAAGAMFLERIPRSI 384
 QY 361 PPEVKFNKPFVFLMIQNTKSPFLFMGKVVNPTQK 394
 DB 385 PPEVKFNKPFVFLMIQNTKSPFLFMGKVVNPTQK 418

RESULT 12

AD63536
 ID ADE63536 standard; protein; 418 AA.

AC ADE63536;

DT 29-JAN-2004 (first entry)

DE Human Protein P01009, SEQ ID NO 9480.

KW Human; pain; neuronal tissue; gene therapy;
 KW spinal segmental nerve injury; chronic constriction injury; CCI;
 KW spared nerve injury; SNI; Chung.

OS Homo sapiens.

PN WO2003016475-A2.

PD 27-FEB-2003.

PF 14-AUG-2002; 2002WO-US025765.

PR 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.

XX (GENO) GEN HOSPITAL CORP.

PA (FAHO) BAYER AG.

PI Woolf C, D'urso D, Befort K, Costigan M;

XX WPI; 2003-268312/26.

DR GENBANK; P01009.

XX New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.

XX Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell

CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a human protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 418 AA;

Query Match 98.6%; Score 2003; DB 7; Length 418;

Best Local Similarity 98.5%; Pred. No. 1.4e-155;

Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDPOGDAQAQKTDTSHHDDQDPTFNKIPNLAEFAFSLYRQLAHQSNSTNIFPSPVSIATA 60
 DB 25 EDPOGDAQAQKTDTSHHDDQDPTFNKIPNLAEFAFSLYRQLAHQSNSTNIFPSPVSIATA 84

QY 61 FAMLISLGTAKADTHDEILEGLNPNLTQIPRAQIHGEGFQELLRTLNQDPSQLQTLTNGGLFL 120
 DB 85 FAMLISLGTAKADTHDEILEGLNPNLTQIPRAQIHGEGFQELLRTLNQDPSQLQTLTNGGLFL 144

QY 121 SQGLKLVDPLEVDVKKLYHSEAFVNFVFGDTEQAQKQINDYVEKGTQGIKIVDLVKELDRDT 180
 DB 145 SEGKLVDPLEVDVKKLYHSEAFVNFVFGDTEQAQKQINDYVEKGTQGIKIVDLVKELDRDT 204

QY 181 VPALVNYIYFFKQWEPFVKDTEEDFHVDQVTVTKVPMKRLGFMFNTOHCKKLSWWL 240
 DB 205 VPALVNYIYFFKQWEPFVKDTEEDFHVDQVTVTKVPMKRLGFMFNTOHCKKLSWWL 264

QY 241 LMKYLGNAITAIFFLPDEGKLOHLENLTHDITTKFLENEDRRSASLHLPKLSITGYDLK 300
 DB 265 LMKYLGNAITAIFFLPDEGKLOHLENLTHDITTKFLENEDRRSASLHLPKLSITGYDLK 324

QY 301 SVLGQIGITKVFNSGADLSGVTEEAFLKLSKAVHKAVALTIDEKGTAAAGAMFLERIPRSI 360
 DB 325 SVLGQIGITKVFNSGADLSGVTEEAFLKLSKAVHKAVALTIDEKGTAAAGAMFLERIPRSI 384

QY 361 PPEVKFNKPFVFLMIQNTKSPFLFMGKVVNPTQK 394
 DB 385 PPEVKFNKPFVFLMIQNTKSPFLFMGKVVNPTQK 418

RESULT 13
 ADE63528
 ID ADE63528 standard; protein; 418 AA.

XX ADE63528;

XX 29-JAN-2004 (first entry)

DE Human Protein P01009, SEQ ID NO 9472.

KW Human; pain; neuronal tissue; gene therapy;
 KW spinal segmental nerve injury; chronic constriction injury; CCI;
 KW spared nerve injury; SNI; Chung.

CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX Sequence 418 AA;
SQ
Query Match 98.6%; Score 2003; DB 7; Length 418;
Best Local Similarity 98.5%; Pred. No. 1.4e-155;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 EDPOGDAQAQKTDTSHHDDQDHPFNKIPNLAFAFSLYRQLAQHSNSTNIPFSPVSIATA 60
DB 25 EDPOGDAQAQKTDTSHHDDQDHPFNKIPNLAFAFSLYRQLAQHSNSTNIPFSPVSIATA 84
QY 61 FAMLISLGTAKADTHDEILGELNPNLTOIPEAQIHGEGFQELLRTLNQPSQLQTTGNGLFL 120
DB 85 FAMLISLGTAKADTHDEILGELNPNLTOIPEAQIHGEGFQELLRTLNQPSQLQTTGNGLFL 144
QY 121 SQGLKLVDFKLEDDVKLVHSEAFVNFQDTEQAKQINDYVEKGTQKIVDLVKELDRDT 180
DB 145 SEGKLVDFKLEDDVKLVHSEAFVNFQDTEQAKQINDYVEKGTQKIVDLVKELDRDT 204
QY 181 VPALVNYIFFKGKWERPPEVKDTEBEDFHVQDVTTVKVPMMKRLGNFNIQHCKLSSWYL 240
DB 205 VPALVNYIFFKGKWERPPEVKDTEBEDFHVQDVTTVKVPMMKRLGNFNIQHCKLSSWYL 264
QY 241 LMKYLGNAITAIFPLPDEGKLOHLENELTHDITKPLENEDRRSASLHLPKLSITGYDLK 300
DB 265 LMKYLGNAITAIFPLPDEGKLOHLENELTHDITKPLENEDRRSASLHLPKLSITGYDLK 324
QY 301 SVLGQGITKVFSGADLSGVTEEPAPLKLKSAVKHKAULTIDEKTEAAGAMFLERIPRSI 360
DB 325 SVLGQGITKVFSGADLSGVTEEPAPLKLKSAVKHKAULTIDEKTEAAGAMFLERIPRSI 384
QY 361 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPTGK 394
DB 385 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPTQK 418
RESULT 15
ADE63524
ID ADE63524 standard; protein; 418 AA.
XX ADE63524;
XX
XX 29-JAN-2004 (first entry)
XX Human Protein P01009, SEQ ID NO 9468.
XX Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX Homo sapiens.
XX WO2003016475-A2.
XX
XX 27-FEB-2003.
XX
XX 14-AUG-2002; 2002WO-US025765.
XX
XX 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
XX (GEO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX

PI Woolf C, D'urso D, Befort K, Costigan M;
XX WPI; 2003-268312/26.
DR GENBANK; P01009.
XX
XX New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
XX Claim 1; Page: 1017pp; English.
XX
XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 418 AA;
SQ
Query Match 98.6%; Score 2003; DB 7; Length 418;
Best Local Similarity 98.5%; Pred. No. 1.4e-155;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 EDPOGDAQAQKTDTSHHDDQDHPFNKIPNLAFAFSLYRQLAQHSNSTNIPFSPVSIATA 60
DB 25 EDPOGDAQAQKTDTSHHDDQDHPFNKIPNLAFAFSLYRQLAQHSNSTNIPFSPVSIATA 84
QY 61 FAMLISLGTAKADTHDEILGELNPNLTOIPEAQIHGEGFQELLRTLNQPSQLQTTGNGLFL 120
DB 85 FAMLISLGTAKADTHDEILGELNPNLTOIPEAQIHGEGFQELLRTLNQPSQLQTTGNGLFL 144
QY 121 SQGLKLVDFKLEDDVKLVHSEAFVNFQDTEQAKQINDYVEKGTQKIVDLVKELDRDT 180
DB 145 SEGKLVDFKLEDDVKLVHSEAFVNFQDTEQAKQINDYVEKGTQKIVDLVKELDRDT 204
QY 181 VPALVNYIFFKGKWERPPEVKDTEBEDFHVQDVTTVKVPMMKRLGNFNIQHCKLSSWYL 240
DB 205 VPALVNYIFFKGKWERPPEVKDTEBEDFHVQDVTTVKVPMMKRLGNFNIQHCKLSSWYL 264
QY 241 LMKYLGNAITAIFPLPDEGKLOHLENELTHDITKPLENEDRRSASLHLPKLSITGYDLK 300
DB 265 LMKYLGNAITAIFPLPDEGKLOHLENELTHDITKPLENEDRRSASLHLPKLSITGYDLK 324
QY 301 SVLGQGITKVFSGADLSGVTEEPAPLKLKSAVKHKAULTIDEKTEAAGAMFLERIPRSI 360
DB 325 SVLGQGITKVFSGADLSGVTEEPAPLKLKSAVKHKAULTIDEKTEAAGAMFLERIPRSI 384
QY 361 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPTGK 394
DB 385 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPTQK 418

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Job time : 80 secs

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OM protein - protein search, using sw model

Run on: June 20, 2005, 19:40:45 ; Search time 43 Seconds
(without alignments)
683.994 Million cell updates/sec

Title: PDX1
Perfect score: 2032
Sequence: 1 EDPOGDAAQKDTSHHDQH.....IEQNTKSLFMGKVNPTRGK 394

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Issued Patents AA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2026	99.7	394	3	US-08-481-534-11
3	2021	99.5	394	1	US-08-002-202-9
4	2020	99.4	394	3	US-08-481-534-6
5	2015	99.2	394	1	US-08-002-202-11
6	2009	98.9	394	1	US-08-002-202-6
7	2003	98.6	394	3	US-09-023-339-1
8	2003	98.6	418	1	US-08-121-714-3
9	2003	98.6	418	1	US-08-477-108A-3
10	2003	98.6	418	2	US-08-477-112-3
11	2003	98.6	418	4	US-10-030-330-3
12	2003	98.6	418	5	PCT-US93-08322-3
13	1993	98.1	418	4	US-10-000-489-92
14	1992	98.0	394	2	US-08-553-488A-1
15	1973	97.1	414	1	US-08-002-202-19
16	1973	97.1	414	3	US-08-481-534-19
17	1967	96.8	414	1	US-08-002-202-13
18	1967	96.8	414	3	US-08-481-534-13
19	1961	96.5	414	1	US-08-002-202-17
20	1961	96.5	414	3	US-08-481-534-17
21	1714	84.4	363	4	US-09-755-665-58
22	1665.5	82.0	351	4	US-10-000-489-50
23	1371	67.5	308	1	US-07-859-480-2
24	1157.5	57.0	421	4	US-09-949-016-8165
25	1125	55.4	420	4	US-09-949-016-6705
26	833	41.0	423	4	US-09-976-594-19
27	833	41.0	423	4	US-09-919-039-19

28	824	40.6	414	4	US-09-949-016-8143	Sequence 8143, Ap
29	811.5	39.9	405	1	US-07-823-954-2	Sequence 2, Appli
30	811.5	39.9	405	1	US-07-994-423-2	Sequence 2, Appli
31	811.5	39.9	405	1	US-08-421-891-2	Sequence 2, Appli
32	811.5	39.9	416	4	US-09-949-016-7597	Sequence 7597, Ap
33	804	39.6	422	4	US-09-244-111-8	Sequence 8, Appli
34	791	38.9	414	4	US-09-755-665-14	Sequence 14, Appli
35	791	38.9	414	4	US-09-755-665-55	Sequence 55, Appli
36	791	38.9	414	4	US-09-755-665-56	Sequence 56, Appli
37	791	38.9	415	4	US-09-461-325-134	Sequence 134, App
38	791	38.9	415	4	US-10-012-542-134	Sequence 134, App
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40	781.5	38.5	419	4	US-09-949-016-11541	Sequence 11541, A
41	775.5	38.2	415	4	US-09-919-039-390	Sequence 390, App
42	767	37.7	361	4	US-09-755-665-57	Sequence 57, Appli
43	752.5	37.0	435	4	US-09-912-628-5	Sequence 5, Appli
44	620	30.5	144	4	US-09-513-999C-4202	Sequence 4202, Ap
45	546.5	26.9	436	3	US-08-660-347-2	Sequence 2, Appli
46	541.5	26.6	444	3	US-09-271-608-8	Sequence 8, Appli
47	541.5	26.6	444	3	US-09-695-950-8	Sequence 8, Appli
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49	541.5	26.6	444	3	US-09-696-364-8	Sequence 8, Appli
50	535.5	26.4	390	4	US-08-731-566-2	Sequence 2, Appli
51	528.5	26.0	390	1	US-08-568-147B-2	Sequence 2, Appli
52	524.5	25.8	390	3	US-09-266-910-3	Sequence 3, Appli
53	522.5	25.7	390	3	US-09-266-910-4	Sequence 4, Appli
54	518	25.5	135	4	US-09-513-999C-7821	Sequence 7821, Ap
55	507.5	25.0	376	1	US-08-464-148-4	Sequence 4, Appli
56	507.5	25.0	376	1	US-08-385-500-4	Sequence 4, Appli
57	507.5	25.0	376	1	US-08-846-784-4	Sequence 4, Appli
58	507	25.0	366	3	US-09-716-793A-2	Sequence 2, Appli
59	495.5	24.4	376	3	US-09-200-965-2	Sequence 2, Appli
60	494.5	24.3	382	1	US-07-768-286B-6	Sequence 6, Appli
61	494.5	24.3	382	1	US-08-487-823B-3	Sequence 3, Appli
62	494.5	24.3	382	2	US-08-997-040-3	Sequence 3, Appli
63	494.5	24.3	382	2	US-09-203-237-3	Sequence 3, Appli
64	492.5	24.2	311	4	US-09-912-628-6	Sequence 6, Appli
65	491.5	24.2	392	1	US-07-768-286B-4	Sequence 4, Appli
66	487	24.0	415	3	US-09-026-408-4	Sequence 4, Appli
67	487	24.0	415	4	US-09-903-684-4	Sequence 4, Appli
68	481	23.7	415	1	US-07-911-531-19	Sequence 19, Appli
69	481	23.7	415	1	US-07-693-636A-19	Sequence 19, Appli
70	481	23.7	415	1	US-07-768-286B-2	Sequence 2, Appli
71	481	23.7	434	1	US-07-679-052A-15	Sequence 15, Appli
72	481	23.7	438	1	US-07-679-052A-17	Sequence 17, Appli
73	480.5	23.6	425	4	US-10-024-427-2	Sequence 2, Appli
74	480	23.6	375	1	US-08-121-714-8	Sequence 8, Appli
75	480	23.6	375	1	US-08-477-108A-8	Sequence 8, Appli
76	480	23.6	375	2	US-08-477-112-8	Sequence 8, Appli
77	480	23.6	375	5	PCT-US93-08322-8	Sequence 8, Appli
78	475.5	23.4	374	1	US-08-464-148-2	Sequence 2, Appli
79	475.5	23.4	374	1	US-08-385-500-2	Sequence 2, Appli
80	475.5	23.4	374	1	US-08-846-784-2	Sequence 2, Appli
81	475.5	23.4	386	4	US-08-545-573A-39	Sequence 39, Appli
82	475	23.4	409	4	US-09-613-303-55	Sequence 55, Appli
83	475	23.4	409	4	US-10-267-311-55	Sequence 55, Appli
84	468.5	23.1	499	4	US-09-054-272-36	Sequence 36, Appli
85	468.5	23.1	499	4	US-09-054-272-51	Sequence 51, Appli
86	468.5	23.1	505	3	US-09-257-581-5	Sequence 5, Appli
87	468.5	23.1	505	3	US-09-257-581-7	Sequence 7, Appli
88	468.5	23.1	520	3	US-09-949-016-10847	Sequence 10847, A
89	468.5	23.1	948	4	US-09-613-303-21	Sequence 21, Appli
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92	467	23.0	405	1	US-08-477-108A-7	Sequence 7, Appli
93	467	23.0	405	2	US-08-477-112-7	Sequence 7, Appli
94	467	23.0	405	5	PCT-US93-08322-3	Sequence 3, Appli
95	465	22.9	410	3	US-09-348-817A-7	Sequence 7, Appli
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98	461	22.7	410	3	US-09-348-817A-2	Sequence 2, Appli
99	461	22.7	410	3	US-09-722-292-2	Sequence 2, Appli
100	456	22.4	402	3	US-08-948-997-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-08-481-534-9
; Sequence 9, Application US/08481534
; Patent No. 6022855
; GENERAL INFORMATION:
; APPLICANT: Thomas, Gary
; APPLICANT: Anderson, Eric D
; APPLICANT: Thomas, Laurel
; APPLICANT: Hayflick, Joel S
; APPLICANT: Nelson, Jay
; APPLICANT: Stenglen, Stephan G
; TITLE OF INVENTION: Methods and Reagents for Inhibiting Furin
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,534
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6022855nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,448-D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 394 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Modified site
; LOCATION: 355..358
; OTHER INFORMATION: /label=Variant
; OTHER INFORMATION: / note="The amino acid sequence is the amino acid
; OTHER INFORMATION: sequence of the modified alpha-1-antitrypsin
; OTHER INFORMATION: protein, alpha-1-antitrypsin Portland."

US-08-481-534-9
Query Match 100.0%; Score 2032; DB 3; Length 394;
Best Local Similarity 100.0%; Pred. No. 6.4e-184;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	EDPQGAQKTTSHHDDHPTFNKITPNLAFSLYRQLAHQSNSTNIFPSPVSIATA 60
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QY	61	FAMLSGTGKADTHDELEGINFLNLTQIPRAQHEGFQELLRLTNOPDSQLOLTGNGLFL 120
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DB	121	SGQLKLVDFKLEVDVKLYHSEAFVTNFGDTEQAKQINDYVEKGTQGIKIVLVKELDRDT 180

QY	181	VFALVNYIFFFKGKWERPFEVKDTEBEDFHVQVTTVKVPMKRLGMFNIQHCKKLSWWL 240
DB	181	VFALVNYIFFFKGKWERPFEVKDTEBEDFHVQVTTVKVPMKRLGMFNIQHCKKLSWWL 240
QY	241	LMKYLGNATAIFFLPDEGKLOHLENELTHDITTKPLENEDRRSASLHLPKLSITGTYDLK 300
DB	241	LMKYLGNATAIFFLPDEGKLOHLENELTHDITTKPLENEDRRSASLHLPKLSITGTYDLK 300
QY	301	SVLGOLGITTKVFSNGADLSGVTEEAPLKLKSAVHKAVLTIDKGTAAAGAMFLERIPRSI 360
DB	301	SVLGOLGITTKVFSNGADLSGVTEEAPLKLKSAVHKAVLTIDKGTAAAGAMFLERIPRSI 360
QY	361	PPEVKFNKPPFVFLMIEQNTKSPFMGKVVNPTGK 394
DB	361	PPEVKFNKPPFVFLMIEQNTKSPFMGKVVNPTGK 394

RESULT 2
US-08-481-534-11
; Sequence 11, Application US/08481534
; Patent No. 6022855
; GENERAL INFORMATION:
; APPLICANT: Thomas, Gary
; APPLICANT: Anderson, Eric D
; APPLICANT: Thomas, Laurel
; APPLICANT: Hayflick, Joel S
; APPLICANT: Nelson, Jay
; APPLICANT: Stenglen, Stephan G
; TITLE OF INVENTION: Methods and Reagents for Inhibiting Furin
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,534
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6022855nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,448-D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; TELEX:
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 394 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Modified site
; LOCATION: 355..358
; OTHER INFORMATION: /label=Variant
; OTHER INFORMATION: / note="The amino acid sequence is the amino acid
; OTHER INFORMATION: sequence of the modified alpha-1-antitrypsin
; OTHER INFORMATION: protein, alpha-1-antitrypsin Pittsburgh."

US-08-481-534-11
Query Match 99.7%; Score 2026; DB 3; Length 394;
Best Local Similarity 99.7%; Pred. No. 2.4e-183;


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; NAME: No. 602855nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,448-D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 394 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-481-534-6

Query Match 99.4%; Score 2020; DB 3; Length 394;
Best Local Similarity 99.5%; Pred. No. 8.8e-183;
Matches 392; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 61 FAMLISLGTAKADTHDEILEGNLNLTOIPEAQIHEGFQELLRLTNOPDSQQLTGTGGLFL 120
Db 61 FAMLISLGTAKADTHDEILEGNLNLTOIPEAQIHEGFQELLRLTNOPDSQQLTGTGGLFL 120
QY 121 SOGLKLVDFKEDVKLYHSEAFVNFVGTQEAQKQINDYVEKGTQGIKIVLVKELDRDT 180
Db 121 SOGLKLVDFKEDVKLYHSEAFVNFVGTQEAQKQINDYVEKGTQGIKIVLVKELDRDT 180
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Db 121 SOGLKLVDFKEDVKLYHSEAFVNFVGTQEAQKQINDYVEKGTQGIKIVLVKELDRDT 180
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Db 181 VFALVNYIFFKQKWRPFVVKDTEREDFHVDQVTVTKVPMKRLGMFNIQHCKLSSWVL 240
QY 241 LMKYLGNAATAIFFLPDEGKLQHLENELTHDITTKFLENEDRRSASLHLPKLSITGYDILK 300
Db 241 LMKYLGNAATAIFFLPDEGKLQHLENELTHDITTKFLENEDRRSASLHLPKLSITGYDILK 300
QY 301 SVLGQGITKVFNSGADLSGVTEEAAPLKLKAVHKAVLTIDEKGTAAAGAMFLERIPRSI 360
Db 301 SVLGQGITKVFNSGADLSGVTEEAAPLKLKAVHKAVLTIDEKGTAAAGAMFLERIPRSI 360
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Db 361 PPEVFNKPFVFLMIEQNTKSPFLMGKVVNPTGK 394

RESULT 5
US-08-002-202-11
; Sequence 11, Application US/08002202
; Patent No. 5604201
; GENERAL INFORMATION:
; APPLICANT: Thomas, Garry
; APPLICANT: Anderson, Eric D
; APPLICANT: Thomas, Laurel
; APPLICANT: Hayflick, Joel S
; TITLE OF INVENTION: Methods and Reagents for Inhibiting
; TITLE OF INVENTION: Furin Endoprotease
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti and Witcoff, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

; NAME: No. 602855nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,448-D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 394 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-481-534-6

Query Match 99.4%; Score 2020; DB 3; Length 394;
Best Local Similarity 99.5%; Pred. No. 8.8e-183;
Matches 392; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 181 VFALVNYIFFKQKWRPFVVKDTEREDFHVDQVTVTKVPMKRLGMFNIQHCKLSSWVL 240
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RESULT 6
US-08-002-202-6
; Sequence 6, Application US/08002202
; Patent No. 5604201
; GENERAL INFORMATION:
; APPLICANT: Thomas, Garry
; APPLICANT: Anderson, Eric D
; APPLICANT: Thomas, Laurel
; APPLICANT: Hayflick, Joel S
; TITLE OF INVENTION: Methods and Reagents for Inhibiting
; TITLE OF INVENTION: Furin Endoprotease
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti and Witcoff, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/002,202
; FILING DATE: 08-JAN-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5604201nan, Kevin E
; REGISTRATION NUMBER: 35,30003
; REFERENCE/DOCKET NUMBER: 92,448
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 394 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1-394
; OTHER INFORMATION: /label= Variants
; OTHER INFORMATION: /note= "This amino acid sequence is the amino acid
; OTHER INFORMATION: sequence of the modified alpha-1-antitrypsin
; OTHER INFORMATION: variant, alpha-1-antitrypsin Pittsburgh "
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STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/002,202
FILING DATE: 08-JAN-1993
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: No. 5604201nan, Kevin E
REGISTRATION NUMBER: 35,30003
REFERENCE/DOCKET NUMBER: 92,448
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 394 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-002-202-6

Query Match 98.9%; Score 2009; DB 1; Length 394;
Best Local Similarity 99.0%; Pred. No. 9.7e-182;
Matches 390; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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DB 301 SVLGQIGITKVFSGNADLSGVTEEAAPLKLKAVHKAVALTIDKGTAAAGAMFLERIPMSI 360
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DB 361 PPEVKFNKPPFVFLMIEQNTKSPFLFMGKVVNPTQK 394

RESULT 7
US-09-023-339-1
Sequence 1, Application US/09023339
Patent No. 6127145
GENERAL INFORMATION:
APPLICANT: Sutliff, Thomas D.
APPLICANT: Rodriguez, Raymond L.
TITLE OF INVENTION: Production of '1-Antitrypsin
TITLE OF INVENTION: in Plants
NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: P.O. Box 60850
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,339
FILING DATE: 13-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/037,991
FILING DATE: 13-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Petithory, Joanne R
REGISTRATION NUMBER: P42,995
REFERENCE/DOCKET NUMBER: 0665-0003.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
TELEFAX: 650-324-0960
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 394 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: mature AAT amino acid sequence
US-09-023-339-1

Query Match 98.6%; Score 2003; DB 3; Length 394;
Best Local Similarity 98.5%; Pred. No. 3.6e-181;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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DB 1 EDPOGDAQKTDTSHHDQDHPFNKITPNLAFAFSLYRQLAHQSNSTNIFSPVSIATA 60
QY 61 FAMLSTGKADTHDEILEGNFNLTQIPEAQIHEGFQELLRTLNQDPSQLQTTGNGFL 120
DB 61 FAMLSTGKADTHDEILEGNFNLTQIPEAQIHEGFQELLRTLNQDPSQLQTTGNGFL 120
QY 121 SOGLKLVDFLEDKVKKLYHSEAFVNFQDTEQAKQINDYVEKGTQGIKIVDLVKELDRDT 180
DB 121 SOGLKLVDFLEDKVKKLYHSEAFVNFQDTEQAKQINDYVEKGTQGIKIVDLVKELDRDT 180
QY 181 VFALVNYIFFKGKWRPFVKDTEEDFHVDOVTVKVPMMKRLGMFNIQHCKLSSWVL 240
DB 181 VFALVNYIFFKGKWRPFVKDTEEDFHVDOVTVKVPMMKRLGMFNIQHCKLSSWVL 240
QY 241 LMKYLGNATAIFPLPDEGKQLHLENLTHDITKPLENEDRRSASLHLPKLSITGYDLK 300
DB 241 LMKYLGNATAIFPLPDEGKQLHLENLTHDITKPLENEDRRSASLHLPKLSITGYDLK 300
QY 301 SVLGQIGITKVFSGNADLSGVTEEAAPLKLKAVHKAVALTIDKGTAAAGAMFLERIPRSI 360
DB 301 SVLGQIGITKVFSGNADLSGVTEEAAPLKLKAVHKAVALTIDKGTAAAGAMFLERIPMSI 360
QY 361 PPEVKFNKPPFVFLMIEQNTKSPFLFMGKVVNPTGK 394
DB 361 PPEVKFNKPPFVFLMIEQNTKSPFLFMGKVVNPTQK 394

RESULT 8
US-08-121-714-3
Sequence 3, Application US/08121714
Patent No. 5470970
GENERAL INFORMATION:

APPLICANT: Sager, Ruth
TITLE OF INVENTION: MASPIN, A NOVEL SERPIN WITH
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/121,714
FILING DATE: 02/28/91
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/938,823
FILING DATE: 09/01/92
APPLICATION NUMBER: 07/844,296
FILING DATE: 02/28/92
APPLICATION NUMBER: 07/662,216
FILING DATE: 02/28/91
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00530/072001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 418
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-121-714-3

Query Match 98.6%; Score 2003; DB 1; Length 418;
Best Local Similarity 98.5%; Pred. No. 3.9e-181;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDPQGDAAQKTDTHSHDQDHPFNKITPNLAEPFSLYRQLAHQSNSTNIFSPVSIATA 60
DB 25 EDPQGDAAQKTDTHSHDQDHPFNKITPNLAEPFSLYRQLAHQSNSTNIFSPVSIATA 84
QY 61 FAWLSLGTADTHDEILGLNENLTIPEAQIHEGFQELLRLTNQDPSQLQTTGNGLFL 120
DB 85 FAWLSLGTADTHDEILGLNENLTIPEAQIHEGFQELLRLTNQDPSQLQTTGNGLFL 144
QY 121 SGLKLVDFLEDDVKLYHSEAFVNFQDTEAKQINDYVEKGTQKIVDLVKELDRDT 180
DB 145 SGLKLVDFLEDDVKLYHSEAFVNFQDTEAKQINDYVEKGTQKIVDLVKELDRDT 204
QY 181 VFALVNYIFFKQWPERPFVKTEEDHFVDQVTTVKVPMKRLGMFNTOHCKKLSWWYL 240
DB 205 VFALVNYIFFKQWPERPFVKTEEDHFVDQVTTVKVPMKRLGMFNTOHCKKLSWWYL 264
QY 241 LMKYLGNAITAPLPDEGKLOHLENLTHDIITKFLNEDRRSASLHLPKLSITGYDLK 300
DB 265 LMKYLGNAITAPLPDEGKLOHLENLTHDIITKFLNEDRRSASLHLPKLSITGYDLK 324
QY 301 SVLGQIGITKVFSGNADLSGVTEEAFLKLSKAVHKAVLTIDEKGTAAAGMFLERIPRSI 360
DB 325 SVLGQIGITKVFSGNADLSGVTEEAFLKLSKAVHKAVLTIDEKGTAAAGMFLERIPRSI 384
QY 361 PPEVKFNKPFVFLMIQNTKSPFLFMGKVVNPTQK 394

DB 385 PPEVKFNKPFVFLMIQNTKSPFLFMGKVVNPTQK 418

RESULT 9
US-08-477-108A-3
Sequence 3, Application US/08477108A
Patent No. 5801001
GENERAL INFORMATION:
APPLICANT: Sager, Ruth
APPLICANT: Zou, Zhiqiang
APPLICANT: Anisowicz, Anthony
TITLE OF INVENTION: MASPIN, A NOVEL SERPIN WITH
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,108A
FILING DATE: June 7, 1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/121,714
FILING DATE: 09/01/93
APPLICATION NUMBER: 07/938,823
FILING DATE: 09/01/92
APPLICATION NUMBER: 07/844,296
FILING DATE: 02/28/92
APPLICATION NUMBER: 07/662,216
FILING DATE: 02/28/91
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 06570/002002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 418
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-477-108A-3

Query Match 98.6%; Score 2003; DB 1; Length 418;
Best Local Similarity 98.5%; Pred. No. 3.9e-181;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDPQGDAAQKTDTHSHDQDHPFNKITPNLAEPFSLYRQLAHQSNSTNIFSPVSIATA 60
DB 25 EDPQGDAAQKTDTHSHDQDHPFNKITPNLAEPFSLYRQLAHQSNSTNIFSPVSIATA 84
QY 61 FAWLSLGTADTHDEILGLNENLTIPEAQIHEGFQELLRLTNQDPSQLQTTGNGLFL 120
DB 85 FAWLSLGTADTHDEILGLNENLTIPEAQIHEGFQELLRLTNQDPSQLQTTGNGLFL 144
QY 121 SGLKLVDFLEDDVKLYHSEAFVNFQDTEAKQINDYVEKGTQKIVDLVKELDRDT 180
DB 145 SGLKLVDFLEDDVKLYHSEAFVNFQDTEAKQINDYVEKGTQKIVDLVKELDRDT 204
QY 181 VFALVNYIFFKQWPERPFVKTEEDHFVDQVTTVKVPMKRLGMFNTOHCKKLSWWYL 240

Db 205 VPALVNYIPFKGKWERPFVKDTEBEDPHVDQVTTVKVPMKELGMFNIHQCKLSSWVL 264
Qy 241 LMKYLGNAITAFPLPDEGKLOHLENELTHDIIITKPLENEDRRSASLHLPKLSITGTGYDLK 300
Db 265 LMKYLGNAITAFPLPDEGKLOHLENELTHDIIITKPLENEDRRSASLHLPKLSITGTGYDLK 324
Qy 301 SVLGQLGITKVFSGADLSGVTEEAPLKLSKAVHKAVLTIDKGTAAAGAMFLERIPRSI 360
Db 325 SVLGQLGITKVFSGADLSGVTEEAPLKLSKAVHKAVLTIDKGTAAAGAMFLERIPRSI 384
Qy 361 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPTQK 394
Db 385 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPTQK 418

RESULT 10

US-08-477-112-3
; Sequence 3, Application US/08477112
; Patent No. 5905023
; GENERAL INFORMATION:
; APPLICANT: Sager, Ruth
; TITLE OF INVENTION: MASPIN, A NOVEL SERPIN WITH
; TITLE OF INVENTION: TUMOR SUPPRESSING ACTIVITY
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 425 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,112
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/121,714
; FILING DATE: 09/01/93
; APPLICATION NUMBER: 07/938,823
; FILING DATE: 09/01/92
; APPLICATION NUMBER: 07/844,296
; FILING DATE: 02/28/92
; APPLICATION NUMBER: 07/662,216
; FILING DATE: 02/28/91
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 06570/002003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 418
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear

US-08-477-112-3
Query Match 98.6%; Score 2003; DB 2; Length 418;
Best Local Similarity 98.5%; Pred. No. 3.9e-181;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
Qy 1 EDPQGDAAQKTDTSHHDQDHPFNKITPNLAFAFSLYRQLAHQSNSTNIFSPVSIATA 60
Db 25 EDPQGDAAQKTDTSHHDQDHPFNKITPNLAFAFSLYRQLAHQSNSTNIFSPVSIATA 84
Qy 61 FAMLSTGKADTHDEILGLENELTHDIIITKPLENEDRRSASLHLPKLSITGTGYDLK 120
Db 85 FAMLSTGKADTHDEILGLENELTHDIIITKPLENEDRRSASLHLPKLSITGTGYDLK 144
Qy 121 SQGLKLVDFKLEDDVKLYHSEAFVNFVFGDTEAKQINDYVEKGTQGGKIVDLVKELDRDT 180
Db 145 SEGKLVDFKLEDDVKLYHSEAFVNFVFGDTEAKQINDYVEKGTQGGKIVDLVKELDRDT 204
Qy 181 VPALVNYIPFKGKWERPFVKDTEBEDPHVDQVTTVKVPMKELGMFNIHQCKLSSWVL 240
Db 205 VPALVNYIPFKGKWERPFVKDTEBEDPHVDQVTTVKVPMKELGMFNIHQCKLSSWVL 264
Qy 241 LMKYLGNAITAFPLPDEGKLOHLENELTHDIIITKPLENEDRRSASLHLPKLSITGTGYDLK 300
Db 265 LMKYLGNAITAFPLPDEGKLOHLENELTHDIIITKPLENEDRRSASLHLPKLSITGTGYDLK 324
Qy 301 SVLGQLGITKVFSGADLSGVTEEAPLKLSKAVHKAVLTIDKGTAAAGAMFLERIPRSI 360
Db 325 SVLGQLGITKVFSGADLSGVTEEAPLKLSKAVHKAVLTIDKGTAAAGAMFLERIPRSI 384

RESULT 11

US-10-030-330-3
; Sequence 3, Application US/10030330
; Patent No. 6833262
; GENERAL INFORMATION:
; APPLICANT: The University of Georgia Research Foundation, Inc
; TITLE OF INVENTION: A POLYPEPTIDE HAVING AMIDOLYTIC ACTIVITY FOR A SERPIN
; FILE REFERENCE: 235.00210201
; CURRENT APPLICATION NUMBER: US/10/030,330
; CURRENT FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 60/130,436
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-030-330-3

Query Match 98.6%; Score 2003; DB 4; Length 418;
Best Local Similarity 98.5%; Pred. No. 3.9e-181;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EDPQGDAAQKTDTSHHDQDHPFNKITPNLAFAFSLYRQLAHQSNSTNIFSPVSIATA 60
Db 25 EDPQGDAAQKTDTSHHDQDHPFNKITPNLAFAFSLYRQLAHQSNSTNIFSPVSIATA 84
Qy 61 FAMLSTGKADTHDEILGLENELTHDIIITKPLENEDRRSASLHLPKLSITGTGYDLK 120
Db 85 FAMLSTGKADTHDEILGLENELTHDIIITKPLENEDRRSASLHLPKLSITGTGYDLK 144
Qy 121 SQGLKLVDFKLEDDVKLYHSEAFVNFVFGDTEAKQINDYVEKGTQGGKIVDLVKELDRDT 180
Db 145 SEGKLVDFKLEDDVKLYHSEAFVNFVFGDTEAKQINDYVEKGTQGGKIVDLVKELDRDT 204
Qy 181 VPALVNYIPFKGKWERPFVKDTEBEDPHVDQVTTVKVPMKELGMFNIHQCKLSSWVL 240
Db 205 VPALVNYIPFKGKWERPFVKDTEBEDPHVDQVTTVKVPMKELGMFNIHQCKLSSWVL 264
Qy 241 LMKYLGNAITAFPLPDEGKLOHLENELTHDIIITKPLENEDRRSASLHLPKLSITGTGYDLK 300
Db 265 LMKYLGNAITAFPLPDEGKLOHLENELTHDIIITKPLENEDRRSASLHLPKLSITGTGYDLK 324
Qy 301 SVLGQLGITKVFSGADLSGVTEEAPLKLSKAVHKAVLTIDKGTAAAGAMFLERIPRSI 360
Db 325 SVLGQLGITKVFSGADLSGVTEEAPLKLSKAVHKAVLTIDKGTAAAGAMFLERIPRSI 384

Qy 361 PPEVFNKPPVFLMIEQNTKSPILFMGKVVNPTGK 394
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Db 385 PPEVFNKPPVFLMIEQNTKSPILFMGKVVNPTOK 418

RESULT 12

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PCT-US93-08322-3
; Sequence 3, Application PC/TUS9308322
; GENERAL INFORMATION:
; APPLICANT: Seger, Ruth
; TITLE OF INVENTION: MASPIN, A NOVEL SERPIN WITH TUMOR SUPPRESSING ACTIVITY
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3 5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08322
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/938,823
; FILING DATE: 09/01/92
; APPLICATION NUMBER: 07/844,296
; FILING DATE: 02/28/92
; APPLICATION NUMBER: 07/662,216
; FILING DATE: 02/28/91
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00530/072001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 418
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
PCT-US93-08322-3

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265	LMKYLGNATAIFFLPDECKLQHLENLTHDIIITKFLNEDRRSSASHLHLPKLSTGTVDLK	324
301	SVLGQLGITKTFKPSNGADLSGVTSEAPLKLKAVHKAVLTIDKGTGAAGMFLERPSI	360
325	SVLGQLGITKTFKPSNGADLSGVTSEAPLKLKAVHKAVLTIDKGTGAAGMFLERPSI	384
361	PPEVFNKPPFVFLMIETQNTKSPFMGKVNPTGK	394
385	PPEVFNKPPFVFLMIETQNTKSPFMGKVNPTOK	418

RESULT 13

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US-10-000-489-92
; Sequence 92, Application US/10000489
; Patent No. 6794363
; GENERAL INFORMATION:
; APPLICANT: Benjamin, Stephane
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 91.US6.DIV
; CURRENT APPLICATION NUMBER: US/10/000,489
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: US 09/924,340
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: PCT/IB01/01715
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: JPatent
; SEQ ID NO 92
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: 1..24
; US-10-000-489-92

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QY 361 PPEVKENKPPVFLMIBQNTKSPKPLFMGKVVNPTGK 394
Db 385 PPEVKENKPPVFLMIBQNTKSPKPLFMGKVVNPTGK 418

RESULT 14
US-08-553-488A-1
; Sequence 1, Application US/08553488A
; Patent No. 5817484
; GENERAL INFORMATION:
; APPLICANT: YU, Myeong-Hee
; APPLICANT: KWON, Ki-Sun
; APPLICANT: LEE, Kee-Nyung
; APPLICANT: SHIN, Hwa-Soo
; TITLE OF INVENTION: THERMORESISTANT ALPHA-1-ANTITRYPSIN
; TITLE OF INVENTION: MUTIN
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YU, Myeong-Hee
; STREET: 3-1003, Hankang Apartment, 49-8, Jamwon-dong,
; STREET: Seocho-gu
; CITY: Seoul
; STATE: Seoul
; COUNTRY: Republic of Korea
; ZIP: 137-030
; ADDRESSEE: KWON, Ki-Sun
; STREET: 130-1306, Hanbit Apartment, Oun-dong,
; STREET: Yuseong-gu
; CITY: Taejeon
; STATE: Taejeon
; COUNTRY: Republic of Korea
; ZIP: 305-333
; ADDRESSEE: LEE, Kee-Nyung
; STREET: 105-1004, Hanbit Apartment, Oun-dong,
; STREET: Yuseong-gu
; CITY: Taejeon
; STATE: Taejeon
; COUNTRY: Republic of Korea
; ZIP: 305-333
; ADDRESSEE: SHIN, Hwa-Soo
; STREET: 3-303, Sindonga Apartment, Yongjeon-dong,
; STREET: Dong-gu
; CITY: Taejeon
; STATE: Taejeon
; COUNTRY: Republic of Korea
; ZIP: 300-200
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5inch, 1.44MB storage
; COMPUTER: IBM PC/AT
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/553,488A
; FILING DATE: 20-NOV-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: KR 93-8510
; FILING DATE: 18-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 394 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; OTHER INFORMATION: wild type human '-1-antitrypsin

US-08-553-488A-1
Query Match 98.0%; Score 1992; DB 2; Length 394;
Best Local Similarity 97.7%; Pred. No. 3.9e-180;
Matches 385; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
QY 1 EDPQGDAAQKTTSHHDQDHPFNKITPNLAEPAFSLYRQLAHQSNSTIFFSPVSIATA 60
Db 1 EDPQGDAAQKTTSHHDQDHPFNKITPNLAEPAFSLYRQLAHQSNSTIFFSPVSIATA 60
QY 61 FAMLISLGTAKADTHDEILEGLNFNLTQIPRAQIHGEGFOELLRTLNQPDLSOLQLTGNGLFL 120
Db 61 FAMLISLGTAKADTHDEILEGLNFNLTQIPRAQIHGEGFOELLRTLNQPDLSOLQLTGNGLFL 120
QY 121 SQGLKLVDKFLKEDVVKLYHSEAFVTNFGDTEQAQKQINDYVEKGTQGIKVDLVKELDRDT 180
Db 121 SEGLKLVDKFLKEDVVKLYHSEAFVTNFGDTEQAQKQINDYVEKGTQGIKVDLVKELDRDT 180
QY 181 VFALVNYIIFPKGKWERPPFVKDTEBEDFHVQDVTTVKVPMMKRLGFMFNIOHCKKLSWVL 240
Db 181 VFALVNYIIFPKGKWERPPFVKDTEBEDFHVQDVTTVKVPMMKRLGFMFNIOHCKKLSWVL 240
QY 241 LMKYLGNAITAFPLPDEGKLOHLENELTHDITTKFLENEEDRRSASLHLPKLSITGYDLK 300
Db 241 LMKYLGNAITAFPLPDEGKLOHLENELTHDITTKFLENEEDRRSASLHLPKLSITGYDLK 300
QY 301 SVLGQLGITKVFNSGADLSGVTEEAPLKLKSKAVHKAULTIDEKGTAAAGAMFLERIPRSI 360
Db 301 SVLGQLGITKVFNSGADLSGVTEEAPLKLKSKAVHKAULTIDEKGTAAAGAMFLERIPRSI 360
QY 361 PPEVKENKPPVFLMIBQNTKSPKPLFMGKVVNPTGK 394
Db 361 PPEVKENKPPVFLMIBQNTKSPKPLFMGKVVNPTGK 394

RESULT 15
US-08-002-202-19
; Sequence 19, Application US/08002202
; Patent No. 5604201
; GENERAL INFORMATION:
; APPLICANT: Thomas, Garry
; APPLICANT: Anderson, Eric D
; APPLICANT: Thomas, Laurel
; APPLICANT: Hayflick, Joel S
; TITLE OF INVENTION: Methods and Reagents for Inhibiting
; TITLE OF INVENTION: Furin Endoprotease
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti and Witcoff, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/002,202
; FILING DATE: 08-JAN-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5604201nan, Kevin E
; REGISTRATION NUMBER: 35,30003
; REFERENCE/DOCKET NUMBER: 92,448
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:

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; LENGTH: 414 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-002-202-19

Query Match          97.1%; Score 1973; DB 1; Length 414;
Best Local Similarity 97.5%; Pred. No. 2.7e-178;
Matches 384; Conservative 4; Mismatches 2; Indels 4; Gaps 1;

QY 1 EDPOGDAQKTDTHHDQDHPFNKITPNLAEFAFSLYRQLAHQSNSTNIFPSPVSIATA 60
Db 25 EDPOGDAQKTDTHHDQDHPFNKITPNLAEFAFSLYRQLAHQSNSTNIFPSPVSIATA 84
QY 61 FAWLSIGTKADTHDEILLEGLENFLTQIPEAQIHEGFOELRLTNQPDSDQLQTTGNGLFL 120
Db 85 FAWLSIGTKADTHDEILLEGLENFLTQIPEAQIHEGFOELRLTN----QLQTTGNGLFL 140
QY 121 SQGLKLVDFKLEDVKKLYHSEAFVNFQDTEQAQKQINDYVEKGTQGKIVDLVVKELDRDT 180
Db 141 SQGLKLVDFKLEDVKKLYHSEAFVNFQDTEQAQKQINDYVEKGTQGKIVDLVVKELDRDT 200
QY 181 VFALVNIYIPFKGKWRPPEVKDTEBEDFHVDQVTTVKVPMKRLGMFNIQHCKKLSSWYL 240
Db 201 VFALVNIYIPFKGKWRPPEVKDTEBEDFHVDQVTTVKVPMKRLGMFNIQHCKKLSSWYL 260
QY 241 LMKYLGNTAIPFLPDEGKLQHLENELTHDIIITKPLENEDRRSASLHLPKLSITGTYDLK 300
Db 261 LMKYLGNTAMFPLPDEGKLQHLENELTHDIIITKPLENEDRRSASLHLPKLSITGTYDLK 320
QY 301 SVLGQLGITKVFSGNADLSGVTEEAPLKLKSAVHKAVLTIDEKGTAAAGAMFLERIPRSI 360
Db 321 SVLGQLGITKVFSGNADLSGVTEEAPLKLKSAVHKAVLTIDEKGTAAAGAMFLERIPRSI 380
QY 361 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVNVPTGK 394
Db 381 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVNVPTGK 414
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Search completed: June 20, 2005, 19:47:29
Job time : 46 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2005, 19:46:00 ; Search time 160 Seconds
(without alignments)

Title: PDX1
 Perfect score: 2032
 Sequence: 1 EDPOGDAAGKTDTSHHDDH.....IEONTKSLFMGKVVNPTGK 394

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1714042 seqs, 383979560 residues

Total number of hits satisfying chosen parameters: 1714042

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

Published_Applications AA:*

- 1: /cgm2_6/ptodata/2/pubpaa/US07_PUBCOMB.pcp.*
- 2: /cgm2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pcp.*
- 3: /cgm2_6/ptodata/2/pubpaa/US05_NEW_PUB.pcp.*
- 4: /cgm2_6/ptodata/2/pubpaa/US06_PUBCOMB.pcp.*
- 5: /cgm2_6/ptodata/2/pubpaa/US07_NEW_PUB.pcp.*
- 6: /cgm2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pcp.*
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- 8: /cgm2_6/ptodata/2/pubpaa/US08_PUBCOMB.pcp.*
- 9: /cgm2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pcp.*
- 10: /cgm2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pcp.*
- 11: /cgm2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pcp.*
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- 13: /cgm2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pcp.*
- 14: /cgm2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pcp.*
- 15: /cgm2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pcp.*
- 16: /cgm2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pcp.*
- 17: /cgm2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pcp.*
- 18: /cgm2_6/ptodata/2/pubpaa/US10_NEW_PUB.pcp.*
- 19: /cgm2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pcp.*
- 20: /cgm2_6/ptodata/2/pubpaa/US11_NEW_PUB.pcp.*
- 21: /cgm2_6/ptodata/2/pubpaa/US60_NEW_PUB.pcp.*
- 22: /cgm2_6/ptodata/2/pubpaa/US60_PUBCOMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SIMMARTES

Result No.	Score	Query #		Length	DB	ID	Description
		Match					
1	2003	98.6	394	14	US-10-025-514-2		Sequence 2, Appli
2	2003	98.6	395	17	US-10-914-863-2		Sequence 2, Appli
3	2003	98.6	418	14	US-10-097-340-286		Sequence 286, App
4	2003	98.6	418	15	US-10-411-037-22		Sequence 22, Appl
5	2003	98.6	418	15	US-10-411-026-22		Sequence 22, Appl
6	2003	98.6	418	15	US-10-410-962-22		Sequence 22, Appl
7	2003	98.6	418	15	US-10-411-049-22		Sequence 22, Appl
8	2003	98.6	418	15	US-10-410-930-22		Sequence 22, Appl
9	2003	98.6	418	16	US-10-410-997-22		Sequence 22, Appl
10	2003	98.6	418	16	US-10-411-012-22		Sequence 22, Appl
11	2003	98.6	418	16	US-10-287-994-22		Sequence 22, Appl

85 827 40.7 423 10 US-09-978-418-14 Sequence 14, Appl
86 827 40.7 423 17 US-10-485-231-14 Sequence 14, Appl
87 824 40.6 379 14 US-10-097-340-139 Sequence 139, App
88 824 40.6 406 17 US-10-741-600-1211 Sequence 1211, Ap
89 824 40.6 406 17 US-10-741-600-1212 Sequence 1212, Ap
90 824 40.6 406 17 US-10-741-600-1213 Sequence 1213, Ap
91 824 40.6 406 17 US-10-741-600-1214 Sequence 1214, Ap
92 824 40.6 406 17 US-10-741-600-1215 Sequence 1215, Ap
93 820 40.4 427 14 US-10-005-956-578 Sequence 578, App
94 819 40.3 411 15 US-10-210-172-122 Sequence 122, App
95 819 40.3 411 15 US-10-210-172-124 Sequence 124, App
96 819 40.3 411 15 US-10-210-172-126 Sequence 126, App
97 819 40.3 411 15 US-10-210-172-128 Sequence 128, App
98 819 40.3 411 15 US-10-210-172-130 Sequence 130, App
99 819 40.3 411 15 US-10-210-172-132 Sequence 132, App
100 819 40.3 411 15 US-10-210-172-134 Sequence 134, App

ALIGNMENTS

RESULT 1
US-10-025-514-2
; Sequence 2, Application US/10025514
; Publication No. US20030073217A1
; GENERAL INFORMATION:
; APPLICANT: Philip J. BARR
; APPLICANT: Helen GIBSON
; APPLICANT: Philip PEMBERTON
; TITLE OF INVENTION: MULTIFUNCTIONAL PROTEASE INHIBITORS AND
; TITLE OF INVENTION: THEIR USE IN TREATMENT OF DISEASE
; FILE REFERENCE: 36829200200
; CURRENT APPLICATION NUMBER: US/10/025,514
; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: U.S. 60/256,699
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: U.S. 60/331,966
; PRIOR FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-025-514-2

Query Match 98.6%; Score 2003; DB 14; Length 394;
Best Local Similarity 98.5%; Pred. No. 2.5e-154;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDPQGDAAQKTDTSHHDDQDHPFNKITPNLAEFAFSLYRQLAHQSNSTNIFPSPVSIATA 60
Db 1 EDPQGDAAQKTDTSHHDDQDHPFNKITPNLAEFAFSLYRQLAHQSNSTNIFPSPVSIATA 60

QY 61 FAMLSTGKTADTHDEILEGNLNFNLTOIPEAQIHEGFQELLRLTNOPDSQLQTTGNGLFL 120
Db 61 FAMLSTGKTADTHDEILEGNLNFNLTOIPEAQIHEGFQELLRLTNOPDSQLQTTGNGLFL 120

QY 121 SQGLKLVDFLEDKVLYHSEAFVNFQGTDEAKQINDYVEKGTQGIKIVDLVKELDRDT 180
Db 121 SQGLKLVDFLEDKVLYHSEAFVNFQGTDEAKQINDYVEKGTQGIKIVDLVKELDRDT 180

QY 181 VFALVNYIFFKGKWERPFVKDTEEDFHVQDQVTTVKVPMKRLGMFNIQHCKLSSWVL 240
Db 181 VFALVNYIFFKGKWERPFVKDTEEDFHVQDQVTTVKVPMKRLGMFNIQHCKLSSWVL 240

QY 241 LMKYLGNAITAFPLPDEGKLOHLENELTHDITTKFLENEDRRSASLHLPKLSITGTIDLK 300
Db 241 LMKYLGNAITAFPLPDEGKLOHLENELTHDITTKFLENEDRRSASLHLPKLSITGTIDLK 300

QY 301 SVLGQLGITKVFNSGADLSGVTEEAAPLKLKSAVHKAVLTIDEKGTAAAGAMFLERIPRSI 360
Db 301 SVLGQLGITKVFNSGADLSGVTEEAAPLKLKSAVHKAVLTIDEKGTAAAGAMFLERIPMSI 360

QY 361 PPEVFNKPFVFLMIEQNTKSPFLFMGKVVNPTGK 394
Db 361 PPEVFNKPFVFLMIEQNTKSPFLFMGKVVNPTGK 394

RESULT 2
US-10-914-863-2
; Sequence 2, Application US/10914863
; Publication No. US20050084972A1
; GENERAL INFORMATION:
; APPLICANT: BARR, PHILIP J.
; APPLICANT: GIBSON, HELEN L.
; TITLE OF INVENTION: METHODS OF PROTEIN PRODUCTION IN YEAST
; FILE REFERENCE: 39042-0012
; CURRENT APPLICATION NUMBER: US/10/914,863
; CURRENT FILING DATE: 2004-08-09
; PRIOR APPLICATION NUMBER: 60/493,984
; PRIOR FILING DATE: 2003-08-08
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 395
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: amino acid sequence
; OTHER INFORMATION: encoded by rAA expression plasmid pYEP829
US-10-914-863-2

Query Match 98.6%; Score 2003; DB 17; Length 395;
Best Local Similarity 98.5%; Pred. No. 2.6e-154;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDPQGDAAQKTDTSHHDDQDHPFNKITPNLAEFAFSLYRQLAHQSNSTNIFPSPVSIATA 60
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QY 61 FAMLSTGKTADTHDEILEGNLNFNLTOIPEAQIHEGFQELLRLTNOPDSQLQTTGNGLFL 120
Db 62 FAMLSTGKTADTHDEILEGNLNFNLTOIPEAQIHEGFQELLRLTNOPDSQLQTTGNGLFL 121

QY 121 SQGLKLVDFLEDKVLYHSEAFVNFQGTDEAKQINDYVEKGTQGIKIVDLVKELDRDT 180
Db 122 SQGLKLVDFLEDKVLYHSEAFVNFQGTDEAKQINDYVEKGTQGIKIVDLVKELDRDT 181

QY 181 VFALVNYIFFKGKWERPFVKDTEEDFHVQDQVTTVKVPMKRLGMFNIQHCKLSSWVL 240
Db 182 VFALVNYIFFKGKWERPFVKDTEEDFHVQDQVTTVKVPMKRLGMFNIQHCKLSSWVL 241

QY 241 LMKYLGNAITAFPLPDEGKLOHLENELTHDITTKFLENEDRRSASLHLPKLSITGTIDLK 300
Db 242 LMKYLGNAITAFPLPDEGKLOHLENELTHDITTKFLENEDRRSASLHLPKLSITGTIDLK 301

QY 301 SVLGQLGITKVFNSGADLSGVTEEAAPLKLKSAVHKAVLTIDEKGTAAAGAMFLERIPRSI 360
Db 302 SVLGQLGITKVFNSGADLSGVTEEAAPLKLKSAVHKAVLTIDEKGTAAAGAMFLERIPMSI 361

QY 361 PPEVFNKPFVFLMIEQNTKSPFLFMGKVVNPTGK 394
Db 362 PPEVFNKPFVFLMIEQNTKSPFLFMGKVVNPTGK 395

RESULT 3
US-10-097-340-286
; Sequence 286, Application US/10097340
; Publication No. US20030087250A1
; GENERAL INFORMATION:
; APPLICANT: John MONAHAN
; APPLICANT: Manjula GANNAVABAPU
; APPLICANT: Sebastian HOERSCH
; APPLICANT: Shubhangi KAMATKAR
; APPLICANT: Steve G. KOVATS

APPLICANT: Rachel E. MEYERS
APPLICANT: Michael MORRISBY
APPLICANT: Peter OLANDT
APPLICANT: Ami SEN
APPLICANT: Peter VEIBY
APPLICANT: Gordon B. MILLS
APPLICANT: Robert C. EAST, Jr.
APPLICANT: Karen LU
APPLICANT: Rosemarie SCHMANDT
APPLICANT: Xumei ZHAO
APPLICANT: Karen GLATT

TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification, Assessment, Prevention, and Therapy of Ovarian Cancer

TITLE OF INVENTION: GALACTOSIDASE A

FILE REFERENCE: MRI-030

CURRENT APPLICATION NUMBER: US/10/097,340

CURRENT FILING DATE: 2002-03-14

PRIOR APPLICATION NUMBER: 60/276,025

PRIOR FILING DATE: 2001-03-14

PRIOR APPLICATION NUMBER: 60/325,149

PRIOR FILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: 60/276,026

PRIOR FILING DATE: 2001-03-14

PRIOR APPLICATION NUMBER: 60/324,967

PRIOR FILING DATE: 2001/09/26

PRIOR APPLICATION NUMBER: 60/311,732

PRIOR FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: 60/325,102

PRIOR FILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: 60/323,580

PRIOR FILING DATE: 2001-09-19

NUMBER OF SEQ ID NOS: 363

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 286

LENGTH: 418

TYPE: PRT

ORGANISM: Homo sapiens

US-10-097-340-286

Query Match 98.6%; Score 2003; DB 14; Length 418;
Best Local Similarity 98.5%; Pred. No. 2.8e-154;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDPOGDAAKTDTSHHDQDHPFNKITPNLAFAFSLYQLAHQSNSTNIFSPVSIATA 60
DB 25 EDPOGDAAKTDTSHHDQDHPFNKITPNLAFAFSLYQLAHQSNSTNIFSPVSIATA 84
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DB 85 FAMLISGKADTHDELEGNFNLTOIPEAQIHEGFQELLRTLNQDPSQLQTTGNGLFL 144
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DB 145 SEGLKLVDFLEVDVKLYHSEAFVTFNFGDTEQAQKQINDYVEKGTQGIKIVDLVKELDRDT 204
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DB 205 VFALVNYIFFKQKWERPFVKDTEEDFHVDOVTTVKVPMKRLGMFNIHQCKLSSWVL 264
QY 241 LMKYLGNTAIFFLPDEGKLOHLENELTHDITTKFLENEDRRSASLHLPKLSITGTIDLK 300
DB 265 LMKYLGNTAIFFLPDEGKLOHLENELTHDITTKFLENEDRRSASLHLPKLSITGTIDLK 324
QY 301 SVLGOLGITKVFNSGADLSGVTEEAAPLKLKSAVHKAVALTIDKGTAAAGAMFLERIPRSI 360
DB 325 SVLGOLGITKVFNSGADLSGVTEEAAPLKLKSAVHKAVALTIDKGTAAAGAMFLERIPRSI 384
QY 361 PPEVKFNKPFVFLMIEQNTKSPFMGKVVNPTGK 394
DB 385 PPEVKFNKPFVFLMIEQNTKSPFMGKVVNPTGK 418

RESULT 4

US-10-411-037-22

Sequence 22, Application US/10411026

Sequence 22, Application US/10411037

Publication No. US20040043446A1

GENERAL INFORMATION:

APPLICANT: Neose Technologies, Inc.

APPLICANT: DeFrees, Shawn

APPLICANT: Zopf, David

APPLICANT: Bayer, Robert

APPLICANT: Hakes, David

APPLICANT: Chen, Xi

APPLICANT: Bowe, Caryn

TITLE OF INVENTION: ALPHA GALACTOSIDASE A

TITLE OF INVENTION: GALACTOSIDASE A

FILE REFERENCE: 040853-01-5082

CURRENT APPLICATION NUMBER: US/10/411,037

CURRENT FILING DATE: 2003-04-09

PRIOR APPLICATION NUMBER: US 60/328,523

PRIOR FILING DATE: 2001-10-10

PRIOR APPLICATION NUMBER: US 60/344,692

PRIOR FILING DATE: 2001-10-19

PRIOR APPLICATION NUMBER: US 60/387,292

PRIOR FILING DATE: 2002-06-07

PRIOR APPLICATION NUMBER: US 60/391,777

PRIOR FILING DATE: 2002-06-25

PRIOR APPLICATION NUMBER: US 60/396,594

PRIOR FILING DATE: 2002-07-17

PRIOR APPLICATION NUMBER: US 60/404,249

PRIOR FILING DATE: 2002-08-16

PRIOR APPLICATION NUMBER: US 60/407,527

PRIOR FILING DATE: 2002-08-28

NUMBER OF SEQ ID NOS: 75

SOFTWARE: PatentIn version 3.2

SEQ ID NO 22

LENGTH: 418

TYPE: PRT

ORGANISM: Homo sapiens

US-10-411-037-22

Query Match 98.6%; Score 2003; DB 15; Length 418;

Best Local Similarity 98.5%; Pred. No. 2.8e-154;

Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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DB 25 EDPOGDAAKTDTSHHDQDHPFNKITPNLAFAFSLYQLAHQSNSTNIFSPVSIATA 84
QY 61 FAMLISGKADTHDELEGNFNLTOIPEAQIHEGFQELLRTLNQDPSQLQTTGNGLFL 120
DB 85 FAMLISGKADTHDELEGNFNLTOIPEAQIHEGFQELLRTLNQDPSQLQTTGNGLFL 144
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DB 205 VFALVNYIFFKQKWERPFVKDTEEDFHVDOVTTVKVPMKRLGMFNIHQCKLSSWVL 264
QY 241 LMKYLGNTAIFFLPDEGKLOHLENELTHDITTKFLENEDRRSASLHLPKLSITGTIDLK 300
DB 265 LMKYLGNTAIFFLPDEGKLOHLENELTHDITTKFLENEDRRSASLHLPKLSITGTIDLK 324
QY 301 SVLGOLGITKVFNSGADLSGVTEEAAPLKLKSAVHKAVALTIDKGTAAAGAMFLERIPRSI 360
DB 325 SVLGOLGITKVFNSGADLSGVTEEAAPLKLKSAVHKAVALTIDKGTAAAGAMFLERIPRSI 384
QY 361 PPEVKFNKPFVFLMIEQNTKSPFMGKVVNPTGK 394
DB 385 PPEVKFNKPFVFLMIEQNTKSPFMGKVVNPTGK 418

RESULT 5

US-10-411-026-22

Sequence 22, Application US/10411026

Publication No. US20040063911A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Defrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; TITLE OF INVENTION: PROTEIN REMODELING METHODS AND PEPTIDES PRODUCED BY THE
; FILE REFERENCE: 040853-01-5053
; CURRENT APPLICATION NUMBER: US/10/411,026
; PRIOR FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-411-026-22

Query Match 98.6%; Score 2003; DB 15; Length 418;
Best Local Similarity 98.5%; Pred. No. 2.8e-154;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
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DB 25 EDPOGDAQAQKTDTHSHDDHPTFNKITPNLAFAFSLYRQLAHQSNSTNIFPSPVSIATA 84
QY 61 FAMLSTGKADTHDEILEGLNPNLTOIPEAQIHEGFQELLRTLNQDPSQLQTTGNGLFL 120
DB 85 FAMLSTGKADTHDEILEGLNPNLTOIPEAQIHEGFQELLRTLNQDPSQLQTTGNGLFL 144
QY 121 SGLKLVDKFLVDVKKLYHSEAFVTNFGDTEQAQKQINDYVEKGTQGIKIVDLVKELDRDT 180
DB 145 SGLKLVDKFLVDVKKLYHSEAFVTNFGDTEQAQKQINDYVEKGTQGIKIVDLVKELDRDT 204
QY 181 VFALVNYIFFKGKWRPPEVKDTEEDFHVQDQVTTVKVPMKRLGMFNIOHCKKLSWWYL 240
DB 205 VFALVNYIFFKGKWRPPEVKDTEEDFHVQDQVTTVKVPMKRLGMFNIOHCKKLSWWYL 264
QY 241 LMKYLGNAITAFPLPDEGKLQLENELTHDITTKFLENEDRRSASLHLPKLSITGYDULK 300
DB 265 LMKYLGNAITAFPLPDEGKLQLENELTHDITTKFLENEDRRSASLHLPKLSITGYDULK 324
QY 301 SVLGQIGITKVFSGADLSGVTEEAAPLKLKSAVHKAVLTIDKGTGAAGAMFLERIPRSI 360
DB 325 SVLGQIGITKVFSGADLSGVTEEAAPLKLKSAVHKAVLTIDKGTGAAGAMFLERIPRSI 384
QY 361 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVNPQTK 394
DB 385 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVNPQTK 418

RESULT 6
US-10-410-962-22
; Sequence 22, Application US/10410962
; Publication No. US20040077836A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.

APPLICANT: Neose Technologies, Inc.
; APPLICANT: Defrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; TITLE OF INVENTION: GRANULOCYTE COLONY STIMULATING FACTOR: REMODELING AND
; FILE REFERENCE: 040853-01-5054
; CURRENT APPLICATION NUMBER: US/10/410,962
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-410-962-22

Query Match 98.6%; Score 2003; DB 15; Length 418;
Best Local Similarity 98.5%; Pred. No. 2.8e-154;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 EDPOGDAQAQKTDTHSHDDHPTFNKITPNLAFAFSLYRQLAHQSNSTNIFPSPVSIATA 60
DB 25 EDPOGDAQAQKTDTHSHDDHPTFNKITPNLAFAFSLYRQLAHQSNSTNIFPSPVSIATA 84
QY 61 FAMLSTGKADTHDEILEGLNPNLTOIPEAQIHEGFQELLRTLNQDPSQLQTTGNGLFL 120
DB 85 FAMLSTGKADTHDEILEGLNPNLTOIPEAQIHEGFQELLRTLNQDPSQLQTTGNGLFL 144
QY 121 SGLKLVDKFLVDVKKLYHSEAFVTNFGDTEQAQKQINDYVEKGTQGIKIVDLVKELDRDT 180
DB 145 SGLKLVDKFLVDVKKLYHSEAFVTNFGDTEQAQKQINDYVEKGTQGIKIVDLVKELDRDT 204
QY 181 VFALVNYIFFKGKWRPPEVKDTEEDFHVQDQVTTVKVPMKRLGMFNIOHCKKLSWWYL 240
DB 205 VFALVNYIFFKGKWRPPEVKDTEEDFHVQDQVTTVKVPMKRLGMFNIOHCKKLSWWYL 264
QY 241 LMKYLGNAITAFPLPDEGKLQLENELTHDITTKFLENEDRRSASLHLPKLSITGYDULK 300
DB 265 LMKYLGNAITAFPLPDEGKLQLENELTHDITTKFLENEDRRSASLHLPKLSITGYDULK 324
QY 301 SVLGQIGITKVFSGADLSGVTEEAAPLKLKSAVHKAVLTIDKGTGAAGAMFLERIPRSI 360
DB 325 SVLGQIGITKVFSGADLSGVTEEAAPLKLKSAVHKAVLTIDKGTGAAGAMFLERIPRSI 384
QY 361 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVNPQTK 394
DB 385 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVNPQTK 418

RESULT 7
US-10-411-049-22
; Sequence 22, Application US/10411049
; Publication No. US20040082026A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.

APPLICANT: DeFrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
APPLICANT: Chen, Xi
APPLICANT: Bowe, Caryn
TITLE OF INVENTION: INTERFERON ALPHA: REMODELING AND GLYCOCONJUGATION OF INTERFERON
FILE REFERENCE: 040853-01-5055
CURRENT APPLICATION NUMBER: US/10/411,049
CURRENT FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/387,292
PRIOR FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR FILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn version 3.2
SEQ ID NO 22
LENGTH: 418
TYPE: PRT
ORGANISM: Homo sapiens
US-10-411-049-22

Query Match 98.6%; Score 2003; DB 15; Length 418;
Best Local Similarity 98.5%; Pred. No. 2.8e-154;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDPOGDAQAQKTDTSHHDDQHPFNKITPNLAFSLYRQLAHQSNSTNIFSPVSIATA 60
DB 25 EDPOGDAQAQKTDTSHHDDQHPFNKITPNLAFSLYRQLAHQSNSTNIFSPVSIATA 84

QY 61 FAWLSGKTADTHDEILEGLNENLTIPEAQIHEGFOELLRTLNQPSQLQTTGNGLFL 120
DB 85 FAWLSGKTADTHDEILEGLNENLTIPEAQIHEGFOELLRTLNQPSQLQTTGNGLFL 144

QY 121 SOGLKLVDFKEDVVKLYHSEAFVNFVGDTEQAKQINDYVEKGTQGIKIVDLVKELDRDT 180
DB 145 SEGLKLVDFKEDVVKLYHSEAFVNFVGDTEQAKQINDYVEKGTQGIKIVDLVKELDRDT 204

QY 181 VPALVNYIPFKGKWRPPEVKDTEBEDPHVDQVTTVKVPMKRLGMFNIOHCKLSSWYL 240
DB 205 VPALVNYIPFKGKWRPPEVKDTEBEDPHVDQVTTVKVPMKRLGMFNIOHCKLSSWYL 264

QY 241 LMKYLGNAITAFPLPDEGKLOHLENELTHDIITKPLENEDRRSASLHLPKLSITGTIDYDK 300
DB 265 LMKYLGNAITAFPLPDEGKLOHLENELTHDIITKPLENEDRRSASLHLPKLSITGTIDYDK 324

QY 301 SVLGOLGITKVPFNSGADLSGVTEEAPLKLKAVHKAVALTIDEKTEAAGAMFLERIPRSI 360
DB 325 SVLGOLGITKVPFNSGADLSGVTEEAPLKLKAVHKAVALTIDEKTEAAGAMFLERIPRSI 384

QY 361 PPEVFNKFPFVFLMIEQNTKSPFLFMGKVVNPTGK 394
DB 385 PPEVFNKFPFVFLMIEQNTKSPFLFMGKVVNPTGK 418

RESULT 8
US-10-410-930-22
Sequence 22, Application US/10410930
Publication No. US20040115168A1
GENERAL INFORMATION:
APPLICANT: Neose Technologies, Inc.
APPLICANT: DeFrees, Shawn

APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
APPLICANT: Chen, Xi
APPLICANT: Bowe, Caryn
TITLE OF INVENTION: INTERFERON BETA: REMODELING AND GLYCOCONJUGATION OF INTERFERON
FILE REFERENCE: 040853-01-5056
CURRENT APPLICATION NUMBER: US/10/410,930
CURRENT FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/387,292
PRIOR FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR FILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn version 3.2
SEQ ID NO 22
LENGTH: 418
TYPE: PRT
ORGANISM: Homo sapiens
US-10-410-930-22

Query Match 98.6%; Score 2003; DB 16; Length 418;
Best Local Similarity 98.5%; Pred. No. 2.8e-154;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDPOGDAQAQKTDTSHHDDQHPFNKITPNLAFSLYRQLAHQSNSTNIFSPVSIATA 60
DB 25 EDPOGDAQAQKTDTSHHDDQHPFNKITPNLAFSLYRQLAHQSNSTNIFSPVSIATA 84

QY 61 FAWLSGKTADTHDEILEGLNENLTIPEAQIHEGFOELLRTLNQPSQLQTTGNGLFL 120
DB 85 FAWLSGKTADTHDEILEGLNENLTIPEAQIHEGFOELLRTLNQPSQLQTTGNGLFL 144

QY 121 SOGLKLVDFKEDVVKLYHSEAFVNFVGDTEQAKQINDYVEKGTQGIKIVDLVKELDRDT 180
DB 145 SEGLKLVDFKEDVVKLYHSEAFVNFVGDTEQAKQINDYVEKGTQGIKIVDLVKELDRDT 204

QY 181 VPALVNYIPFKGKWRPPEVKDTEBEDPHVDQVTTVKVPMKRLGMFNIOHCKLSSWYL 240
DB 205 VPALVNYIPFKGKWRPPEVKDTEBEDPHVDQVTTVKVPMKRLGMFNIOHCKLSSWYL 264

QY 241 LMKYLGNAITAFPLPDEGKLOHLENELTHDIITKPLENEDRRSASLHLPKLSITGTIDYDK 300
DB 265 LMKYLGNAITAFPLPDEGKLOHLENELTHDIITKPLENEDRRSASLHLPKLSITGTIDYDK 324

QY 301 SVLGOLGITKVPFNSGADLSGVTEEAPLKLKAVHKAVALTIDEKTEAAGAMFLERIPRSI 360
DB 325 SVLGOLGITKVPFNSGADLSGVTEEAPLKLKAVHKAVALTIDEKTEAAGAMFLERIPRSI 384

QY 361 PPEVFNKFPFVFLMIEQNTKSPFLFMGKVVNPTGK 394
DB 385 PPEVFNKFPFVFLMIEQNTKSPFLFMGKVVNPTGK 418

RESULT 9
US-10-410-997-22
Sequence 22, Application US/10410997
Publication No. US20040126838A1
GENERAL INFORMATION:
APPLICANT: Neose Technologies, Inc.
APPLICANT: DeFrees, Shawn
APPLICANT: Zopf, David

; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryn
; TITLE OF INVENTION: FOLLICLE STIMULATING HORMONE: REMODELING AND GLYCOCONJUGATION OF
; FILE REFERENCE: 040853-01-5059
; CURRENT APPLICATION NUMBER: US/10/410,997
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-410-997-22

Query Match 98.6%; Score 2003; DB 16; Length 418;
Best Local Similarity 98.5%; Pred. No. 2.8e-154;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDPOGDAQAQKTDTHSHDQDHPFNKITPNLAFAFSLYRQLAHQSNSTNIFSPVSIATA 60
DB 25 EDPOGDAQAQKTDTHSHDQDHPFNKITPNLAFAFSLYRQLAHQSNSTNIFSPVSIATA 84
QY 61 FAMLISGKTADTHDEILEGNLNLTOIPEAQIHEGFOELLRTLNOPDSOLQTTGNGLFL 120
DB 85 FAMLISGKTADTHDEILEGNLNLTEIPEAQIHEGFOELLRTLNOPDSOLQTTGNGLFL 144
QY 121 SGLKLVDFKEDVKKLYHSEAFVNFQDTEAKQINDYVEKGTQKIVDLVKELDRDT 180
DB 145 SGLKLVDFKEDVKKLYHSEAFVNFQDTEAKQINDYVEKGTQKIVDLVKELDRDT 204
QY 181 VPALVNYIFFKGKWRPFVVKDTEBEDFHVQDQVTTVKVPMKRLGMFNIQHCKLSSWYL 240
DB 205 VPALVNYIFFKGKWRPFVVKDTEBEDFHVQDQVTTVKVPMKRLGMFNIQHCKLSSWYL 264
QY 241 LMKYLGNATAIFLPDEGKLOHLENLTHDITTKFLENEDRRSASLHLPKLSITGYDJK 300
DB 265 LMKYLGNATAIFLPDEGKLOHLENLTHDITTKFLENEDRRSASLHLPKLSITGYDJK 324
QY 301 SVLGOLGITKVFSGNADLSGVTEEAPLKLKSAVHKAVLTIDSKGTEAAGAMFLERIPRSI 360
DB 325 SVLGOLGITKVFSGNADLSGVTEEAPLKLKSAVHKAVLTIDSKGTEAAGAMFLERIPRSI 384
QY 361 PPEVFNKPFVFLMIEQNTKSPFLFMGKVVNPTQK 394
DB 385 PPEVFNKPFVFLMIEQNTKSPFLFMGKVVNPTQK 418

RESULT 10
US-10-411-012-22
; Sequence 22, Application US/10411012
; Publication No. US20040132640A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert

; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryn
; TITLE OF INVENTION: GLYCOPEGYLATION METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE
; FILE REFERENCE: 040853-01-5051
; CURRENT APPLICATION NUMBER: US/10/411,012
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-411-012-22

Query Match 98.6%; Score 2003; DB 16; Length 418;
Best Local Similarity 98.5%; Pred. No. 2.8e-154;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDPOGDAQAQKTDTHSHDQDHPFNKITPNLAFAFSLYRQLAHQSNSTNIFSPVSIATA 60
DB 25 EDPOGDAQAQKTDTHSHDQDHPFNKITPNLAFAFSLYRQLAHQSNSTNIFSPVSIATA 84
QY 61 FAMLISGKTADTHDEILEGNLNLTOIPEAQIHEGFOELLRTLNOPDSOLQTTGNGLFL 120
DB 85 FAMLISGKTADTHDEILEGNLNLTEIPEAQIHEGFOELLRTLNOPDSOLQTTGNGLFL 144
QY 121 SGLKLVDFKEDVKKLYHSEAFVNFQDTEAKQINDYVEKGTQKIVDLVKELDRDT 180
DB 145 SGLKLVDFKEDVKKLYHSEAFVNFQDTEAKQINDYVEKGTQKIVDLVKELDRDT 204
QY 181 VPALVNYIFFKGKWRPFVVKDTEBEDFHVQDQVTTVKVPMKRLGMFNIQHCKLSSWYL 240
DB 205 VPALVNYIFFKGKWRPFVVKDTEBEDFHVQDQVTTVKVPMKRLGMFNIQHCKLSSWYL 264
QY 241 LMKYLGNATAIFLPDEGKLOHLENLTHDITTKFLENEDRRSASLHLPKLSITGYDJK 300
DB 265 LMKYLGNATAIFLPDEGKLOHLENLTHDITTKFLENEDRRSASLHLPKLSITGYDJK 324
QY 301 SVLGOLGITKVFSGNADLSGVTEEAPLKLKSAVHKAVLTIDSKGTEAAGAMFLERIPRSI 360
DB 325 SVLGOLGITKVFSGNADLSGVTEEAPLKLKSAVHKAVLTIDSKGTEAAGAMFLERIPRSI 384
QY 361 PPEVFNKPFVFLMIEQNTKSPFLFMGKVVNPTQK 394
DB 385 PPEVFNKPFVFLMIEQNTKSPFLFMGKVVNPTQK 418

RESULT 11
US-10-287-994-22
; Sequence 22, Application US/10287994
; Publication No. US20040137557A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Bowe, Caryn

; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; TITLE OF INVENTION: REMODELING AND GLYCOCONJUGATION OF PEPTIDES
; FILE REFERENCE: 040853-01-5052-00
; CURRENT APPLICATION NUMBER: US/10/287,994
; CURRENT FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-994-22

Query Match 98.6%; Score 2003; DB 16; Length 418;
Best Local Similarity 98.5%; Pred. No. 2.8e-154;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 EDPOGDAQAQKTDTSHHDDQDHTFNKITPNLAFAFSLYRQLAHQSNSTNIFSPVSIATA 60
DB 25 EDPOGDAQAQKTDTSHHDDQDHTFNKITPNLAFAFSLYRQLAHQSNSTNIFSPVSIATA 84
QY 61 FAMLSTGKADTHDEILEGNFNLTQIPEAQIHEGFQELLRTLNQDPSQLTGTGNGLFL 120
DB 85 FAMLSTGKADTHDEILEGNFNLTQIPEAQIHEGFQELLRTLNQDPSQLTGTGNGLFL 144
QY 121 SQGLKLVDFLEVDKVLHSEAFVNFQDTEAQKQINDYVEKGTQCKIVDLVKELDROT 180
DB 145 SEGKLVDFLEVDKVLHSEAFVNFQDTEAQKQINDYVEKGTQCKIVDLVKELDROT 204
QY 181 VFALVNYIFFKGKWERPFVKDTEEDFHDVQVTTVKVPMKRLGMFNIQHCKKLSWVL 240
DB 205 VFALVNYIFFKGKWERPFVKDTEEDFHDVQVTTVKVPMKRLGMFNIQHCKKLSWVL 264
QY 241 LMKYLGNAITAIFLPDEGKLOHLENLTHDITTKFLENERDRSASLHLPKLSITGTGYDLK 300
DB 265 LMKYLGNAITAIFLPDEGKLOHLENLTHDITTKFLENERDRSASLHLPKLSITGTGYDLK 324
QY 301 SVLGQGITKVFSGNADLSGVTEAPLKLKSAVHKAVLTIDEKGTAAAGAMFLERIPRSI 360
DB 325 SVLGQGITKVFSGNADLSGVTEAPLKLKSAVHKAVLTIDEKGTAAAGAMFLERIPRSI 384
QY 361 PPEVKFNKPFVFLMIQNQTSKPLFMGKVVNPTGK 394
DB 385 PPEVKFNKPFVFLMIQNQTSKPLFMGKVVNPTGK 418

RESULT 12
US-10-410-913-22
; Sequence 22, Application US/10410913
; Publication No. US20040142856A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryn

; TITLE OF INVENTION: GLYCOCONJUGATION METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE
; TITLE OF INVENTION: METHODS
; FILE REFERENCE: 040853-01-5081
; CURRENT APPLICATION NUMBER: US/10/410,913
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-410-913-22

Query Match 98.6%; Score 2003; DB 16; Length 418;
Best Local Similarity 98.5%; Pred. No. 2.8e-154;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 EDPOGDAQAQKTDTSHHDDQDHTFNKITPNLAFAFSLYRQLAHQSNSTNIFSPVSIATA 60
DB 25 EDPOGDAQAQKTDTSHHDDQDHTFNKITPNLAFAFSLYRQLAHQSNSTNIFSPVSIATA 84
QY 61 FAMLSTGKADTHDEILEGNFNLTQIPEAQIHEGFQELLRTLNQDPSQLTGTGNGLFL 120
DB 85 FAMLSTGKADTHDEILEGNFNLTQIPEAQIHEGFQELLRTLNQDPSQLTGTGNGLFL 144
QY 121 SQGLKLVDFLEVDKVLHSEAFVNFQDTEAQKQINDYVEKGTQCKIVDLVKELDROT 180
DB 145 SEGKLVDFLEVDKVLHSEAFVNFQDTEAQKQINDYVEKGTQCKIVDLVKELDROT 204
QY 181 VFALVNYIFFKGKWERPFVKDTEEDFHDVQVTTVKVPMKRLGMFNIQHCKKLSWVL 240
DB 205 VFALVNYIFFKGKWERPFVKDTEEDFHDVQVTTVKVPMKRLGMFNIQHCKKLSWVL 264
QY 241 LMKYLGNAITAIFLPDEGKLOHLENLTHDITTKFLENERDRSASLHLPKLSITGTGYDLK 300
DB 265 LMKYLGNAITAIFLPDEGKLOHLENLTHDITTKFLENERDRSASLHLPKLSITGTGYDLK 324
QY 301 SVLGQGITKVFSGNADLSGVTEAPLKLKSAVHKAVLTIDEKGTAAAGAMFLERIPRSI 360
DB 325 SVLGQGITKVFSGNADLSGVTEAPLKLKSAVHKAVLTIDEKGTAAAGAMFLERIPRSI 384
QY 361 PPEVKFNKPFVFLMIQNQTSKPLFMGKVVNPTGK 394
DB 385 PPEVKFNKPFVFLMIQNQTSKPLFMGKVVNPTGK 418

RESULT 13
US-10-410-980-22
; Sequence 22, Application US/10410980
; Publication No. US20050031584A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryn
; TITLE OF INVENTION: INTERLEUKIN-2: REMODELING AND GLYCOCONJUGATION OF IL-2


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; FILE REFERENCE: 040853-01-5066
; CURRENT APPLICATION NUMBER: US/10/410,980
; PRIOR FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-410-980-22

Query Match          98.6%; Score 2003; DB 17; Length 418;
Best Local Similarity 98.5%; Pred. No. 2.8e-154;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDPOGDAQAQKTDTSHHDDQHPFTFNKITPNLAFSAFSLYRQLAHQSNSTNIFSPVSIATA 60
DB 25 EDPOGDAQAQKTDTSHHDDQHPFTFNKITPNLAFSAFSLYRQLAHQSNSTNIFSPVSIATA 84
QY 61 FAMLISGTTKADTHDEILEGNFNLTQIPEAQIHEGFQELLRTLNQDPSQLQTTGNGLFL 120
DB 85 FAMLISGTTKADTHDEILEGNFNLTQIPEAQIHEGFQELLRTLNQDPSQLQTTGNGLFL 144
QY 121 SOGLKLVDFLEVDVKLYHSEAFVNFNGDTEEAQKQINDYVEKGTQGIKIVDLVKELDRDT 180
DB 145 SEGKLVDFLEVDVKLYHSEAFVNFNGDTEEAQKQINDYVEKGTQGIKIVDLVKELDRDT 204
QY 181 VFALVNYIFFKGKWERPFVKDTEEDFHVDQVTTVKVPMKRLGMFNIQHCKKLSWWVL 240
DB 205 VFALVNYIFFKGKWERPFVKDTEEDFHVDQVTTVKVPMKRLGMFNIQHCKKLSWWVL 264
QY 241 LMKYLGNAITAIFFLPDEGKQLHLENELTHDIIITKFLNEDRRSASLHLPKLSITGTYDLK 300
DB 265 LMKYLGNAITAIFFLPDEGKQLHLENELTHDIIITKFLNEDRRSASLHLPKLSITGTYDLK 324
QY 301 SVLGQGITKTVFSNGADLSGVTEEAAPLKLKSAVHKAVLTIDEKGTAAAGAMFLERIPRSI 360
DB 325 SVLGQGITKTVFSNGADLSGVTEEAAPLKLKSAVHKAVLTIDEKGTAAAGAMFLERIPMSI 384
QY 361 PPEVKFNKPFVFLMIQNTKSPLEFMGKVVNPTGK 394
DB 385 PPEVKFNKPFVFLMIQNTKSPLEFMGKVVNPTQK 418

RESULT 14
US-10-971-461-15
; Sequence 15, Application US/10971461
; Publication No. US20050070477A1
; GENERAL INFORMATION:
; APPLICANT: Cochrane, Charles G.
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: Treatment and Prevention of Pulmonary Conditions
; FILE REFERENCE: 1361.037US1
; CURRENT APPLICATION NUMBER: US/10/971,461
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo sapiens
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-971-461-15

Query Match          98.6%; Score 2003; DB 17; Length 418;
Best Local Similarity 98.5%; Pred. No. 2.8e-154;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDPOGDAQAQKTDTSHHDDQHPFTFNKITPNLAFSAFSLYRQLAHQSNSTNIFSPVSIATA 60
DB 25 EDPOGDAQAQKTDTSHHDDQHPFTFNKITPNLAFSAFSLYRQLAHQSNSTNIFSPVSIATA 84
QY 61 FAMLISGTTKADTHDEILEGNFNLTQIPEAQIHEGFQELLRTLNQDPSQLQTTGNGLFL 120
DB 85 FAMLISGTTKADTHDEILEGNFNLTQIPEAQIHEGFQELLRTLNQDPSQLQTTGNGLFL 144
QY 121 SOGLKLVDFLEVDVKLYHSEAFVNFNGDTEEAQKQINDYVEKGTQGIKIVDLVKELDRDT 180
DB 145 SEGKLVDFLEVDVKLYHSEAFVNFNGDTEEAQKQINDYVEKGTQGIKIVDLVKELDRDT 204
QY 181 VFALVNYIFFKGKWERPFVKDTEEDFHVDQVTTVKVPMKRLGMFNIQHCKKLSWWVL 240
DB 205 VFALVNYIFFKGKWERPFVKDTEEDFHVDQVTTVKVPMKRLGMFNIQHCKKLSWWVL 264
QY 241 LMKYLGNAITAIFFLPDEGKQLHLENELTHDIIITKFLNEDRRSASLHLPKLSITGTYDLK 300
DB 265 LMKYLGNAITAIFFLPDEGKQLHLENELTHDIIITKFLNEDRRSASLHLPKLSITGTYDLK 324
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US-10-410-897-22
; Sequence 22, Application US/10410897
; Publication No. US20050100982A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryn
; TITLE OF INVENTION: FACTOR IX; REMODELING AND GLYCOCONJUGATION OF FACTOR IX
; FILE REFERENCE: 040853-01-5058
; CURRENT APPLICATION NUMBER: US/10/410,897
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-10-410-897-22

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GenCore version 5.1.6
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OM protein - protein search, using sw model

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Minimum DB seq length: 0
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Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2026	99.7	394	16	US-09-290-034C-6	Sequence 6, Appli
3	2026	99.7	394	17	US-09-372-003-11	Sequence 11, Appli
4	2021	99.5	394	16	US-09-290-034C-1	Sequence 1, Appli
5	2020	99.4	394	17	US-09-372-003-6	Sequence 2, Appli
6	2003	98.6	394	26	US-10-025-514-2	Sequence 2, Appli
7	2003	98.6	395	35	US-10-914-863-2	Sequence 286, Appli
8	2003	98.6	418	1	PCT-US02-07826-286	Sequence 22, Appli
9	2003	98.6	418	1	PCT-US02-32263-22	Sequence 20, Appli
10	2003	98.6	418	1	PCT-US03-12324-20	Sequence 15, Appli
11	2003	98.6	418	1	PCT-US03-12731-15	Sequence 22, Appli
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81 1999 98.4 418 35 US-10-995-561-759 Sequence 759, App
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83 1999 98.4 418 37 US-60-453-050-11995 Sequence 11995, A
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98 1999 98.4 418 37 US-60-608-498-718 Sequence 718, App
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ALIGNMENTS

RESULT 1
US-09-372-003-9
; Sequence 9, Application US/09372003
; GENERAL INFORMATION:
; APPLICANT: Thomas, Gary
; APPLICANT: Anderson, Eric D
; APPLICANT: Thomas, Laurel
; APPLICANT: Haylick, Joel S
; APPLICANT: Nelson, Jay
; APPLICANT: Stenglen, Stephan G
; TITLE OF INVENTION: Methods and Reagents for Inhibiting Furin
; TITLE OF INVENTION: Endoprotease
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/372,003
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/481,534
; FILING DATE: 14-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Noonan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,448-D
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 394 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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; NAME/KEY: Modified site
; LOCATION: 355..358
; OTHER INFORMATION: /label=Variant
; OTHER INFORMATION: /note="The amino acid sequence is the amino acid
; OTHER INFORMATION: sequence of the modified alpha-1-antitrypsin
; OTHER INFORMATION: protein, alpha-1-antitrypsin Portland."
US-09-372-003-9
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Best Local Similarity 100.0%; Pred. No. 4e-177;
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RESULT 2

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; Sequence 6, Application US/09290034C
; GENERAL INFORMATION:
; APPLICANT: Jean, Francois
; APPLICANT: Thomas, Gary
; TITLE OF INVENTION: Reagents and Methods for Inhibiting Furin Endoprotease
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 92448-H
; CURRENT APPLICATION NUMBER: US/09/290,034C
; CURRENT FILING DATE: 1999-04-08
; PRIOR APPLICATION NUMBER: 60/081,034
; PRIOR FILING DATE: 1998-04-09
; NUMBER OF SEQ ID NOS: 6
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; SEQ ID NO 6
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; TYPE: PRT
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; Sequence 11, Application US/09372003
; GENERAL INFORMATION:
; APPLICANT: Thomas, Gary
; APPLICANT: Anderson, Eric D
; APPLICANT: Thomas, Laurel
; APPLICANT: Haylick, Joel S
; APPLICANT: Nelson, Jay
; APPLICANT: Stenglen, Stephan G
; TITLE OF INVENTION: Methods and Reagents for Inhibiting Furin
; TITLE OF INVENTION: Endoprotease
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/372,003
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/481,534
; FILING DATE: 14-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Noonan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,448-D
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; TELEX:
; INFORMATION FOR SEQ ID NO: 11:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 394 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Modified site
; LOCATION: 355..358 /label=Variant
; OTHER INFORMATION: /note="The amino acid sequence is the amino acid
; OTHER INFORMATION: sequence of the modified alpha-1-antitrypsin
; OTHER INFORMATION: protein, alpha-1-antitrypsin Pittsburgh."
; US-09-372-003-11

Query Match 99.7%; Score 2026; DB 17; Length 394;
Best Local Similarity 99.7%; Pred. No. 1.4e-176;
Matches 393; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDQGGAAQKTDTSHHDQDHPFNKIPNLAEPFSLYRQLAHQSNSTNFFSPVSIATA 60
DB 1 EDQGGAAQKTDTSHHDQDHPFNKIPNLAEPFSLYRQLAHQSNSTNFFSPVSIATA 60
QY 61 FAMLSTGTAKDTHDEILGELNPNLTQIPRAQIHGEGFQELLRTLNQDPSQLQTTGNGLFL 120
DB 61 FAMLSTGTAKDTHDEILGELNPNLTQIPRAQIHGEGFQELLRTLNQDPSQLQTTGNGLFL 120
QY 121 SQGLKLVDFLEVDKVLHSEAFVNFQDTEQAQKQINDYVEKGTQGIQVLDVKELDRDT 180
DB 121 SQGLKLVDFLEVDKVLHSEAFVNFQDTEQAQKQINDYVEKGTQGIQVLDVKELDRDT 180
QY 181 VPALVNYIFPKGKWERPFVKDTEEDFHVQDVTTVKVPMMKRLGMFNIOHCKKLSWVL 240
DB 181 VPALVNYIFPKGKWERPFVKDTEEDFHVQDVTTVKVPMMKRLGMFNIOHCKKLSWVL 240
QY 241 LMKYLGNAITAFPLPDEGKLQHLNELTHDITTKFLENERDRRSASLHLPKLSITGYDVK 300
DB 241 LMKYLGNAITAFPLPDEGKLQHLNELTHDITTKFLENERDRRSASLHLPKLSITGYDVK 300
QY 301 SVLGQGITKVFSGADLSGVTSEAPLKLKSAVHKAVLTIDEKGTAAAGAMFLERIPRSI 360
DB 301 SVLGQGITKVFSGADLSGVTSEAPLKLKSAVHKAVLTIDEKGTAAAGAMFLERIPRSI 360
QY 361 PPEVKFNKPFVFLMIQNTKSPFLFMGKVNNPTGK 394
DB 361 PPEVKFNKPFVFLMIQNTKSPFLFMGKVNNPTGK 394

RESULT 4
US-09-290-034C-1
; Sequence 1, Application US/09290034C
; GENERAL INFORMATION:
; APPLICANT: Jean, Francois
; APPLICANT: Thomas, Gary
; TITLE OF INVENTION: Reagents and Methods for Inhibiting Furin Endoprotease
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 92448-H
; CURRENT APPLICATION NUMBER: US/09/290,034C
; CURRENT FILING DATE: 1999-04-08
; PRIOR APPLICATION NUMBER: 60/081,034
; PRIOR FILING DATE: 1998-04-09
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-290-034C-1

Query Match 99.5%; Score 2021; DB 16; Length 394;
Best Local Similarity 99.5%; Pred. No. 4.1e-176;
Matches 392; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EDQGGAAQKTDTSHHDQDHPFNKIPNLAEPFSLYRQLAHQSNSTNFFSPVSIATA 60
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Db 1 EDPQGDAAQKTDTSHHDQDHPFNKITPNLAFAFSLYRQLAHQSNSTNIFPSPVSIATA 60
QY 61 FAWLSLGTAKDTHDEILEGNFNLTQIPEAQIHEGFQELLRTLNQDPSQLTTGNGLFL 120
Db 61 FAWLSLGTAKDTHDEILEGNFNLTQIPEAQIHEGFQELLRTLNQDPSQLTTGNGLFL 120
QY 121 SQGLKLVDFLEVDVKLYHSEAFVNFVFGDTEQAQKQINDYVEKGTQCKIVDLVKELDROT 180
Db 121 SQGLKLVDFLEVDVKLYHSEAFVNFVFGDTEQAQKQINDYVEKGTQCKIVDLVKELDROT 180
QY 181 VFALVNYIYFFKGKWERPPEVKDTEEDFHVQDQVTVKVPMMKRLGMFNIQHCKLSSWVL 240
Db 181 VFALVNYIYFFKGKWERPPEVKDTEEDFHVQDQVTVKVPMMKRLGMFNIQHCKLSSWVL 240
QY 241 LMKYLGNAITAIFFLPDEGKLOHLENELTHDIIITKPLENEDRRSASLHLPKLSITGTYDLK 300
Db 241 LMKYLGNAITAIFFLPDEGKLOHLENELTHDIIITKPLENEDRRSASLHLPKLSITGTYDLK 300
QY 301 SVLGQGITKVFSGADLSGVTEEAFLKSKAVHKAVLTIDEKGTAAAGAMFLERIPRSI 360
Db 301 SVLGQGITKVFSGADLSGVTEEAFLKSKAVHKAVLTIDEKGTAAAGAMFLERIPRSI 360
QY 361 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPTGK 394
Db 361 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPTGK 394

RESULT 5
US-09-372-003-6
; Sequence 6, Application US/09372003
; GENERAL INFORMATION:
; APPLICANT: Thomas, Gary
; APPLICANT: Anderson, Eric D
; APPLICANT: Thomas, Laurel
; APPLICANT: Haylick, Joel S
; APPLICANT: Nelson, Jay
; APPLICANT: Stenglen, Stephan G
; TITLE OF INVENTION: Methods and Reagents for Inhibiting Furin
; TITLE OF INVENTION: Endoprotease
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/372,003
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/481,534
; FILING DATE: 14-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Noonan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,448-D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 394 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

; MOLECULE TYPE: protein
US-09-372-003-6
Query Match 99.4%; Score 2020; DB 17; Length 394;
Best Local Similarity 99.5%; Pred. No. 5.1e-176;
Matches 392; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 EDPQGDAAQKTDTSHHDQDHPFNKITPNLAFAFSLYRQLAHQSNSTNIFPSPVSIATA 60
Db 1 EDPQGDAAQKTDTSHHDQDHPFNKITPNLAFAFSLYRQLAHQSNSTNIFPSPVSIATA 60
QY 61 FAWLSLGTAKDTHDEILEGNFNLTQIPEAQIHEGFQELLRTLNQDPSQLTTGNGLFL 120
Db 61 FAWLSLGTAKDTHDEILEGNFNLTQIPEAQIHEGFQELLRTLNQDPSQLTTGNGLFL 120
QY 121 SQGLKLVDFLEVDVKLYHSEAFVNFVFGDTEQAQKQINDYVEKGTQCKIVDLVKELDROT 180
Db 121 SQGLKLVDFLEVDVKLYHSEAFVNFVFGDTEQAQKQINDYVEKGTQCKIVDLVKELDROT 180
QY 181 VFALVNYIYFFKGKWERPPEVKDTEEDFHVQDQVTVKVPMMKRLGMFNIQHCKLSSWVL 240
Db 181 VFALVNYIYFFKGKWERPPEVKDTEEDFHVQDQVTVKVPMMKRLGMFNIQHCKLSSWVL 240
QY 241 LMKYLGNAITAIFFLPDEGKLOHLENELTHDIIITKPLENEDRRSASLHLPKLSITGTYDLK 300
Db 241 LMKYLGNAITAIFFLPDEGKLOHLENELTHDIIITKPLENEDRRSASLHLPKLSITGTYDLK 300
QY 301 SVLGQGITKVFSGADLSGVTEEAFLKSKAVHKAVLTIDEKGTAAAGAMFLERIPRSI 360
Db 301 SVLGQGITKVFSGADLSGVTEEAFLKSKAVHKAVLTIDEKGTAAAGAMFLERIPRSI 360
QY 361 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPTGK 394
Db 361 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPTGK 394

RESULT 6
US-10-025-514-2
; Sequence 2, Application US/10025514
; GENERAL INFORMATION:
; APPLICANT: Philip J. BARR
; APPLICANT: Helen GIBSON
; APPLICANT: Philip PEMBERTON
; TITLE OF INVENTION: MULTIFUNCTIONAL PROTEASE INHIBITORS AND
; TITLE OF INVENTION: THEIR USE IN TREATMENT OF DISEASE
; FILE REFERENCE: 368292000200
; CURRENT APPLICATION NUMBER: US/10/025,514
; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: U.S. 60/256,699
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: U.S. 60/331,966
; PRIOR FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-025-514-2

Query Match 98.6%; Score 2003; DB 26; Length 394;
Best Local Similarity 98.5%; Pred. No. 1.9e-174;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 EDPQGDAAQKTDTSHHDQDHPFNKITPNLAFAFSLYRQLAHQSNSTNIFPSPVSIATA 60
Db 1 EDPQGDAAQKTDTSHHDQDHPFNKITPNLAFAFSLYRQLAHQSNSTNIFPSPVSIATA 60
QY 61 FAWLSLGTAKDTHDEILEGNFNLTQIPEAQIHEGFQELLRTLNQDPSQLTTGNGLFL 120
Db 61 FAWLSLGTAKDTHDEILEGNFNLTQIPEAQIHEGFQELLRTLNQDPSQLTTGNGLFL 120
QY 121 SQGLKLVDFLEVDVKLYHSEAFVNFVFGDTEQAQKQINDYVEKGTQCKIVDLVKELDROT 180

Db 121 SEGKLVDFKLEVDKKLYHSEAFVNFEDTEAAKQINDYVEKGTQGIQVLDLVEKLDRT 180
Qy 181 VFALVNYIFFKQKWERPFVKDTEEDFHVQDVQVTVTKVPMKRLGMFNIQHCKKLSWVL 240
Db 181 VFALVNYIFFKQKWERPFVKDTEEDFHVQDVQVTVTKVPMKRLGMFNIQHCKKLSWVL 240
Qy 241 LMKYLGNAITAFPLPDEGKLOHLENLTHDIIITKFLNEDRRSASLHLPKLSITGYDLK 300
Db 241 LMKYLGNAITAFPLPDEGKLOHLENLTHDIIITKFLNEDRRSASLHLPKLSITGYDLK 300
Qy 301 SVLGQIGITKVFNSGADLSGVTEAPLKLKSAVHKAVLTIDEKGTAAAGAMFLERIPRSI 360
Db 301 SVLGQIGITKVFNSGADLSGVTEAPLKLKSAVHKAVLTIDEKGTAAAGAMFLERIPMSI 360
Qy 361 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPQK 394
Db 361 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPQK 394
RESULT 7
US-10-914-863-2
; Sequence 2, Application US/10914863
; GENERAL INFORMATION:
; APPLICANT: GIBSON, HELEN L.
; APPLICANT: BARR, PHILIP J.
; TITLE OF INVENTION: METHODS OF PROTEIN PRODUCTION IN YEAST
; FILE REFERENCE: 39042-0012
; CURRENT APPLICATION NUMBER: US/10/914,863
; CURRENT FILING DATE: 2004-08-09
; PRIOR APPLICATION NUMBER: 60/493,984
; PRIOR FILING DATE: 2003-08-08
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 395
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: amino acid sequence
; OTHER INFORMATION: encoded by rAA expression plasmid pYEP829
US-10-914-863-2
Query Match 98.6%; Score 2003; DB 35; Length 395;
Best Local Similarity 98.5%; Pred. No. 1.9e-174;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
Qy 1 EDQGDAAQKTDTSHHDQDPTFNKITPNLAEPFSLYRQLAHQSNSTNIFPSPVSIATA 60
Db 2 EDQGDAAQKTDTSHHDQDPTFNKITPNLAEPFSLYRQLAHQSNSTNIFPSPVSIATA 61
Qy 61 FAMLSTGTAKDTHDEILEGLNFNLTQIPEAQIHEGFQELLRTLNQPDQSLQLTGNGLFL 120
Db 62 FAMLSTGTAKDTHDEILEGLNFNLTQIPEAQIHEGFQELLRTLNQPDQSLQLTGNGLFL 121
Qy 121 SQGLKLVDFKLEVDKKLYHSEAFVNFEDTEAAKQINDYVEKGTQGIQVLDLVEKLDRT 180
Db 122 SEGKLVDFKLEVDKKLYHSEAFVNFEDTEAAKQINDYVEKGTQGIQVLDLVEKLDRT 181
Qy 181 VFALVNYIFFKQKWERPFVKDTEEDFHVQDVQVTVTKVPMKRLGMFNIQHCKKLSWVL 240
Db 182 VFALVNYIFFKQKWERPFVKDTEEDFHVQDVQVTVTKVPMKRLGMFNIQHCKKLSWVL 241
Qy 241 LMKYLGNAITAFPLPDEGKLOHLENLTHDIIITKFLNEDRRSASLHLPKLSITGYDLK 300
Db 242 LMKYLGNAITAFPLPDEGKLOHLENLTHDIIITKFLNEDRRSASLHLPKLSITGYDLK 301
Qy 301 SVLGQIGITKVFNSGADLSGVTEAPLKLKSAVHKAVLTIDEKGTAAAGAMFLERIPRSI 360
Db 302 SVLGQIGITKVFNSGADLSGVTEAPLKLKSAVHKAVLTIDEKGTAAAGAMFLERIPMSI 361
Qy 361 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPQK 394

Db 362 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPQK 395
RESULT 8
PCT-US02-07826-286
; Sequence 286, Application PC/TUS0207826
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc. et al.
; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
; TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
; FILE REFERENCE: MRI-030PC
; CURRENT APPLICATION NUMBER: PCT/US02/07826
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 60/276,025
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/325,149
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 60/276,026
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/324,967
; PRIOR FILING DATE: 2001/09/26
; PRIOR APPLICATION NUMBER: 60/311,732
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/325,102
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/323,580
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 286
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-07826-286
Query Match 98.6%; Score 2003; DB 1; Length 418;
Best Local Similarity 98.5%; Pred. No. 2.1e-174;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
Qy 1 EDQGDAAQKTDTSHHDQDPTFNKITPNLAEPFSLYRQLAHQSNSTNIFPSPVSIATA 60
Db 25 EDQGDAAQKTDTSHHDQDPTFNKITPNLAEPFSLYRQLAHQSNSTNIFPSPVSIATA 84
Qy 61 FAMLSTGTAKDTHDEILEGLNFNLTQIPEAQIHEGFQELLRTLNQPDQSLQLTGNGLFL 120
Db 85 FAMLSTGTAKDTHDEILEGLNFNLTQIPEAQIHEGFQELLRTLNQPDQSLQLTGNGLFL 144
Qy 121 SQGLKLVDFKLEVDKKLYHSEAFVNFEDTEAAKQINDYVEKGTQGIQVLDLVEKLDRT 180
Db 145 SEGKLVDFKLEVDKKLYHSEAFVNFEDTEAAKQINDYVEKGTQGIQVLDLVEKLDRT 204
Qy 181 VFALVNYIFFKQKWERPFVKDTEEDFHVQDVQVTVTKVPMKRLGMFNIQHCKKLSWVL 240
Db 205 VFALVNYIFFKQKWERPFVKDTEEDFHVQDVQVTVTKVPMKRLGMFNIQHCKKLSWVL 264
Qy 241 LMKYLGNAITAFPLPDEGKLOHLENLTHDIIITKFLNEDRRSASLHLPKLSITGYDLK 300
Db 265 LMKYLGNAITAFPLPDEGKLOHLENLTHDIIITKFLNEDRRSASLHLPKLSITGYDLK 324
Qy 301 SVLGQIGITKVFNSGADLSGVTEAPLKLKSAVHKAVLTIDEKGTAAAGAMFLERIPRSI 360
Db 325 SVLGQIGITKVFNSGADLSGVTEAPLKLKSAVHKAVLTIDEKGTAAAGAMFLERIPMSI 384
Qy 361 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPQK 394
Db 385 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPQK 418
RESULT 9
PCT-US02-32263-22
; Sequence 22, Application PC/TUS0232263
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.

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; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Bowe, Caryn
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; TITLE OF INVENTION: REMODELING AND GLYCOCONJUGATION OF PEPTIDES
; FILE REFERENCE: 040853-01-5050W0
; CURRENT APPLICATION NUMBER: PCT/US02/32263
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/334,233
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/334,301
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 22
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-32263-22
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Query Match      98.6%; Score 2003; DB 1; Length 418;
Best Local Similarity 98.5%; Pred. No. 2.1e-174;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDPOGDAQAQTDTSHHDQDHPFNKITPNLAFAFSLYRQLAHQSNSTNIFPSPVSIATA 60
DB 25 EDPOGDAQAQTDTSHHDQDHPFNKITPNLAFAFSLYRQLAHQSNSTNIFPSPVSIATA 84
QY 61 FAMLSTGKADTHDEILEGLNFNLTQIPRAQIHGFGQELLRTLNQDPSQLQTTGNGLFL 120
DB 85 FAMLSTGKADTHDEILEGLNFNLTQIPRAQIHGFGQELLRTLNQDPSQLQTTGNGLFL 144
QY 121 SOGLKLVDFLEDVKKLYHSEAFVNFNGDTEQAQKQINDYVEKGTQKIVDLVKELDRDT 180
DB 145 SEGKLVDFLEDVKKLYHSEAFVNFNGDTEQAQKQINDYVEKGTQKIVDLVKELDRDT 204
QY 181 VFALVNYIFPKGKWERPFVKDTEEDFHVQDQVTTVKVPMKRLGMFNIQHCKKLSWWL 240
DB 205 VFALVNYIFPKGKWERPFVKDTEEDFHVQDQVTTVKVPMKRLGMFNIQHCKKLSWWL 264
QY 241 LMKYLGNAITAIFFLPDEGKLOHLENELTHDIIITKPLENEDRRSASLHLPKLSITGTGDLK 300
DB 265 LMKYLGNAITAIFFLPDEGKLOHLENELTHDIIITKPLENEDRRSASLHLPKLSITGTGDLK 324
QY 301 SVLGQIGITKVFNSGADLSGVTEEAAPLKLSKAVHKAVLTIDEKGTAAAGAMFLERIPRSI 360
DB 325 SVLGQIGITKVFNSGADLSGVTEEAAPLKLSKAVHKAVLTIDEKGTAAAGAMFLERIPRSI 384
QY 361 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPTGK 394
DB 385 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPTGK 418

RESULT 10
PCT-US03-12324-20
; Sequence 20, Application PC/TUS0312324
; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute
; APPLICANT: Cochran, Charles G.
; APPLICANT: Oades, Zenaïda G.
; APPLICANT: Revak, Susan D.
; APPLICANT: Niven, Ralph
; TITLE OF INVENTION: Treatment and Prevention of Pulmonary Conditions
; FILE REFERENCE: 1361.037W01
; CURRENT APPLICATION NUMBER: PCT/US03/12731
; CURRENT FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: US 60/375,968
; PRIOR FILING DATE: 2002-04-25
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 418
; TYPE: PRT
```

```

; APPLICANT: UNIVERSITY OF FLORIDA
; APPLICANT: ATKINSON, MARK A.
; APPLICANT: FLOTTE, TERENCE R.
; APPLICANT: SONG, SIHONG
; APPLICANT: LOILER, SCOTT A.
; TITLE OF INVENTION: FFAV VECTOR-BASED COMPOSITIONS AND METHODS FOR THE PREVENTION AND
; TITLE OF INVENTION: TREATMENT OF MAMMALIAN DISEASES
; FILE REFERENCE: 4300.014510
; CURRENT APPLICATION NUMBER: PCT/US03/12324
; CURRENT FILING DATE: 2003-04-21
; PRIOR APPLICATION NUMBER: 60/374,083
; PRIOR FILING DATE: 2003-04-19
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 20
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-12324-20

Query Match      98.6%; Score 2003; DB 1; Length 418;
Best Local Similarity 98.5%; Pred. No. 2.1e-174;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDPOGDAQAQTDTSHHDQDHPFNKITPNLAFAFSLYRQLAHQSNSTNIFPSPVSIATA 60
DB 25 EDPOGDAQAQTDTSHHDQDHPFNKITPNLAFAFSLYRQLAHQSNSTNIFPSPVSIATA 84
QY 61 FAMLSTGKADTHDEILEGLNFNLTQIPRAQIHGFGQELLRTLNQDPSQLQTTGNGLFL 120
DB 85 FAMLSTGKADTHDEILEGLNFNLTQIPRAQIHGFGQELLRTLNQDPSQLQTTGNGLFL 144
QY 121 SOGLKLVDFLEDVKKLYHSEAFVNFNGDTEQAQKQINDYVEKGTQKIVDLVKELDRDT 180
DB 145 SEGKLVDFLEDVKKLYHSEAFVNFNGDTEQAQKQINDYVEKGTQKIVDLVKELDRDT 204
QY 181 VFALVNYIFPKGKWERPFVKDTEEDFHVQDQVTTVKVPMKRLGMFNIQHCKKLSWWL 240
DB 205 VFALVNYIFPKGKWERPFVKDTEEDFHVQDQVTTVKVPMKRLGMFNIQHCKKLSWWL 264
QY 241 LMKYLGNAITAIFFLPDEGKLOHLENELTHDIIITKPLENEDRRSASLHLPKLSITGTGDLK 300
DB 265 LMKYLGNAITAIFFLPDEGKLOHLENELTHDIIITKPLENEDRRSASLHLPKLSITGTGDLK 324
QY 301 SVLGQIGITKVFNSGADLSGVTEEAAPLKLSKAVHKAVLTIDEKGTAAAGAMFLERIPRSI 360
DB 325 SVLGQIGITKVFNSGADLSGVTEEAAPLKLSKAVHKAVLTIDEKGTAAAGAMFLERIPRSI 384
QY 361 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPTGK 394
DB 385 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPTGK 418

RESULT 11
PCT-US03-12731-15
; Sequence 15, Application PC/TUS0312731
; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute
; APPLICANT: Cochran, Charles G.
; APPLICANT: Oades, Zenaïda G.
; APPLICANT: Revak, Susan D.
; APPLICANT: Niven, Ralph
; TITLE OF INVENTION: Treatment and Prevention of Pulmonary Conditions
; FILE REFERENCE: 1361.037W01
; CURRENT APPLICATION NUMBER: PCT/US03/12731
; CURRENT FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: US 60/375,968
; PRIOR FILING DATE: 2002-04-25
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 418
; TYPE: PRT
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; ORGANISM: Homo sapiens			
PCT-US03-31974-15			
Query Match		98.6%; Score 2003; DB 1; Length 418;	
Best Local Similarity		98.5%; Pred. No. 2.1e-174;	
Matches 388; Conservative		3; Mismatches 3; Indels 0; Gaps 0;	
QY	1	EDPQGDAAQKTDTS	HHDDHPTFNK
DB	25	EDPQGDAAQKTDTS	HHDDHPTFNK
QY	61	FAMLSGTGKADTHD	ELGLNFTNLT
DB	85	FAMLSGTGKADTHD	ELGLNFTNLT
QY	121	SOGLKLVDFLE	DKVKKLHSEAF
DB	145	SEGLKLVDFLE	DKVKKLHSEAF
QY	181	VFALVNYI	IFPKGWERP
DB	205	VFALVNYI	IFPKGWERP
QY	241	LMKYLGNATAI	FFLPDEGKLH
DB	265	LMKYLGNATAI	FFLPDEGKLH
QY	301	SVLGQGITK	VFSNGADLS
DB	325	SVLGQGITK	VFSNGADLS
QY	361	PPEVKPNK	PFVFLMIEQNT
DB	385	PPEVKPNK	PFVFLMIEQNT
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; Sequence 22, Application PC/TUS0331974			
; GENERAL INFORMATION:			
; APPLICANT: Neose Technologies, Inc.			
; APPLICANT: DeFrees, Shawn			
; APPLICANT: Zopf, David			
; APPLICANT: Bayer, Robert			
; APPLICANT: Hakes, David			
; APPLICANT: Chen, Xi			
; APPLICANT: Bowe, Caryne			
; TITLE OF INVENTION: ERYTHROPOIETIN: REMODELING AND GLYCOCONJUGATION OF			
; FILE REFERENCE: 040853-01-5083WO			
; CURRENT APPLICATION NUMBER: PCT/US03/31974			
; CURRENT FILING DATE: 2003-10-08			
; PRIOR APPLICATION NUMBER: PCT/US02/32263			
; PRIOR FILING DATE: 2002-10-09			
; PRIOR APPLICATION NUMBER: US 10/287,994			
; PRIOR FILING DATE: 2002-11-05			
; PRIOR APPLICATION NUMBER: US 10/360,770			
; PRIOR FILING DATE: 2003-01-06			
; PRIOR APPLICATION NUMBER: US 10/369,779			
; PRIOR FILING DATE: 2003-03-17			
; PRIOR APPLICATION NUMBER: US 10/410,945			
; PRIOR FILING DATE: 2003-04-09			
; NUMBER OF SEQ ID NOS: 75			
; SOFTWARE: Patentin version 3.2			
; SEQ ID NO 22			
; LENGTH: 418			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
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Best Local Similarity		98.5%; Pred. No. 2.1e-174;	
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QY	181	VFALVNYI	IFPKGWERP
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QY	241	LMKYLGNATAI	FFLPDEGKLH
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QY	301	SVLGQGITK	VFSNGADLS
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RESULT 13			
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; Sequence 22, Application PC/TUS0411494			
; GENERAL INFORMATION:			
; APPLICANT: Neose Technologies, Inc.			
; APPLICANT: DeFrees, Shawn			
; APPLICANT: Zopf, David			
; APPLICANT: Bayer, Robert			
; APPLICANT: Hakes, David			
; APPLICANT: Chen, Xi			
; APPLICANT: Bowe, Caryne			
; TITLE OF INVENTION: GLYCOEGLYATION METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE			
; FILE REFERENCE: 040853-01-5051WO			
; CURRENT APPLICATION NUMBER: PCT/US04/11494			
; CURRENT FILING DATE: 2004-04-19			
; PRIOR APPLICATION NUMBER: US 60/328,523			
; PRIOR FILING DATE: 2001-10-10			
; PRIOR APPLICATION NUMBER: US 60/334,233			
; PRIOR FILING DATE: 2001-11-28			
; PRIOR APPLICATION NUMBER: US 60/334,301			
; PRIOR FILING DATE: 2001-11-28			
; PRIOR APPLICATION NUMBER: US 60/344,692			
; PRIOR FILING DATE: 2001-10-19			
; PRIOR APPLICATION NUMBER: US 60/387,292			
; PRIOR FILING DATE: 2002-06-07			
; PRIOR APPLICATION NUMBER: US 60/391,777			
; PRIOR FILING DATE: 2002-06-25			
; PRIOR APPLICATION NUMBER: US 60/396,594			
; PRIOR FILING DATE: 2002-07-17			
; PRIOR APPLICATION NUMBER: US 60/404,249			
; PRIOR FILING DATE: 2002-08-16			
; PRIOR APPLICATION NUMBER: US 60/407,527			
; PRIOR FILING DATE: 2002-08-28			
; PRIOR APPLICATION NUMBER: PCT/US02/32263			
; PRIOR FILING DATE: 2002-10-09			
; Remaining Prior Application data removed - See File Wrapper or PALM.			
; NUMBER OF SEQ ID NOS: 75			
; SOFTWARE: Patentin version 3.2			
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; LENGTH: 418			
; TYPE: PRT			
; ORGANISM: Homo sapiens			

PCT-US04-11494-22

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Best Local Similarity 98.5%; Pred. No. 2.1e-174;
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DB 85 FAWLSGTTKADTHDELEGLNENLTCIPEAQIHEGFOELLRTLNQDPSQLQTTGNGFL 144

QY 121 SOGLKLVDFLEDVKLYHSEAFVNFVGTQTEAKKQINDYVEKGTQGIKIVDLVKELDRDT 180
DB 145 SEGLKLVDFLEDVKLYHSEAFVNFVGTQTEAKKQINDYVEKGTQGIKIVDLVKELDRDT 204

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DB 205 VFALVNYIIPFKGWERPPEVKDTEEREDFHVQDQVTVVKVPMKRLGMFNIQHCKKLSWWL 264

QY 241 LMKYLGNAITAIFFLPDEGKLOHLENELTHDIIITKFLNEDRRSASLHLPKLSITGYDLK 300
DB 265 LMKYLGNAITAIFFLPDEGKLOHLENELTHDIIITKFLNEDRRSASLHLPKLSITGYDLK 324

QY 301 SVLGQIGITKVFNSGADLSGVTEEAPLKLSKAVHKAVALTIDEGKTEAAGAMFLERIPRSI 360
DB 325 SVLGQIGITKVFNSGADLSGVTEEAPLKLSKAVHKAVALTIDEGKTEAAGAMFLERIPRSI 384

QY 361 PPEVKFNKPFVFLMIEQNTKSPLFMGKVNPPTQK 394
DB 385 PPEVKFNKPFVFLMIEQNTKSPLFMGKVNPPTQK 418
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; Sequence 2, Application US/08459292
; GENERAL INFORMATION:
; APPLICANT: Brigham, Kenneth
; APPLICANT: Conary, Jon
; APPLICANT: Canonico, Angelo
; APPLICANT: Meyrick, Barbara
; TITLE OF INVENTION: DNA Construct for In Vivo Expression of
; TITLE OF INVENTION: a Human Gene
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESSES:
; ADDRESSES: Tilton, Fallon, Lungmus & Chestnut
; STREET: 100 South Wacker Drive - Suite 960
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60606-4002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,292
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 690,283
; FILING DATE: 24-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: VU9111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 456-8000
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
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; LENGTH: 418 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-459-292-2

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Best Local Similarity 98.5%; Pred. No. 2.1e-174;
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DB 25 EDPOGDAAKTDTSHHDQDHPFNKITPNLAEPFSLYRQLAHQSNSTNIFSPVSIATA 84

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DB 85 FAWLSGTTKADTHDELEGLNENLTCIPEAQIHEGFOELLRTLNQDPSQLQTTGNGFL 144

QY 121 SOGLKLVDFLEDVKLYHSEAFVNFVGTQTEAKKQINDYVEKGTQGIKIVDLVKELDRDT 180
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QY 181 VFALVNYIIPFKGWERPPEVKDTEEREDFHVQDQVTVVKVPMKRLGMFNIQHCKKLSWWL 240
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DB 325 SVLGQIGITKVFNSGADLSGVTEEAPLKLSKAVHKAVALTIDEGKTEAAGAMFLERIPRSI 384

QY 361 PPEVKFNKPFVFLMIEQNTKSPLFMGKVNPPTQK 394
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RESULT 15
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; Sequence 3, Application US/08472758
; GENERAL INFORMATION:
; APPLICANT: Sager, Ruth
; TITLE OF INVENTION: MASPIN, A NOVEL SERPIN
; TITLE OF INVENTION: WITH
; TITLE OF INVENTION: ACTIVITY
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESSES:
; ADDRESSES: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3 5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,758
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/121,714
; FILING DATE: 09/01/93
; APPLICATION NUMBER: 07/938,823
; FILING DATE: 09/01/92
; APPLICATION NUMBER: 07/844,296
; FILING DATE: 02/28/92
; APPLICATION NUMBER: 07/662,216
; FILING DATE: 02/28/91
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TUMOR SUPPRESSING

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; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 06570/002003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 418
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
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US-08-472-758-3

Query Match      98.6%; Score 2003; DB 8; Length 418;
Best Local Similarity 98.5%; Pred. No. 2,1e-174;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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Qy 85 FAMLSTGKADYTHDEILEGLNFNLITQIPRAQIHGEGQELLRTLNQPSQLQLTGNGLFL 144
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db ||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db ||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy 205 VPALVNYIPFGKWRPPEVKDTEEDFHVQVTTVKVPMKRLGMFNIQHCKKLSWVL 264
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 241 LMKYLGNATAIFFLPDEGKLOHLENELTHDIIITKPLENEDRRSASLHLPKLSITGYDLK 300
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Qy 325 SVLGQLGITKVFNGADLSGVTEAPKLKSKAVHKAVLTIDEKGTAAAGAMFLERIPMSI 384
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 361 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVNPTGK 394
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39.5	406	1	PCT-US05-11532-1164	Sequence 1164, Appl
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37.1	417	6	US-10-179-524-452	Sequence 452, Appl
37.1	417	7	US-11-025-607-236	Sequence 236, Appl
37.1	417	7	US-11-030-653-24	Sequence 24, Appl
37.0	417	7	US-11-030-653-131	Sequence 131, Appl
37.0	417	7	PCT-US05-11532-1156	Sequence 1156, Appl
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26.9	436	1	PCT-US05-11532-1813	Sequence 1813, Appl
26.7	374	1	PCT-US04-05232-44	Sequence 44, Appl
26.7	374	1	PCT-US04-05232A-44	Sequence 44, Appl
26.4	374	1	PCT-US04-05232-46	Sequence 46, Appl
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25.0	376	8	US-60-651-506-239	Sequence 253, Appl
25.0	376	8	US-60-651-506-257	Sequence 257, Appl
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ALIGNMENTS

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RESULT 1
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; Sequence 2, Application PCT/US0507959
; GENERAL INFORMATION:
; APPLICANT: Arriva Pharmaceuticals, Inc.
; TITLE OF INVENTION: TREATMENT OF CHRONIC OBSTRUCTIVE PULMONARY DISEASE BY
; FILE OF INVENTION: LOW DOSE INHALATION OF PROTEASE INHIBITOR
; FILE REFERENCE: 39042-0020 PCT
; CURRENT APPLICATION NUMBER: PCT/US05/07959
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: U.S. 60/551,856
; PRIOR FILING DATE: 2004-03-09
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 2
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Homo sapiens
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Best Local Similarity 98.5%; Pred. No. 1.3e-149; Indels 0; Gaps 0;
Matches 388; Conservative 3; Mismatches 3;

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QY 121 SQGLKLVDFKLEDDVKLYHSEAFVNFQDTEQAQKQINDYVEKGTQGIKIVDLVKELDRDT 180
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QY 181 VPALVNYIFFKGKWERPFVKDTEEDFHDVDQVTTVKVPMKRLGFMNIOHCKKLSWYL 240
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US-11-077-276-2
; Sequence 2, Application US/11077276
; GENERAL INFORMATION:
; APPLICANT: Philip J. BARR
; APPLICANT: Philip PEMBERTON
; APPLICANT: Helen GIBSON
; TITLE OF INVENTION: TREATMENT OF CHRONIC OBSTRUCTIVE PULMONARY DISEASE BY
; FILE OF INVENTION: LOW DOSE INHALATION OF PROTEASE INHIBITOR
; FILE REFERENCE: 39042-0020
; CURRENT APPLICATION NUMBER: US/11/077,276
; CURRENT FILING DATE: 2005-03-09
; PRIOR APPLICATION NUMBER: U.S. 60/551,856
; PRIOR FILING DATE: 2004-03-09
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Db 121 SQGLKLVDFKLEDDVKLYHSEAFVNFQDTEQAQKQINDYVEKGTQGIKIVDLVKELDRDT 180

QY 181 VPALVNYIFFKGKWERPFVKDTEEDFHDVDQVTTVKVPMKRLGFMNIOHCKKLSWYL 240
Db 181 VPALVNYIFFKGKWERPFVKDTEEDFHDVDQVTTVKVPMKRLGFMNIOHCKKLSWYL 240

QY 241 LMKYLGNAATAIFFLPDEGKLQHLNETHDIIITKFLNEDRRSASLHLPKLSITGYDILK 300
Db 241 LMKYLGNAATAIFFLPDEGKLQHLNETHDIIITKFLNEDRRSASLHLPKLSITGYDILK 300

QY 301 SVLGQGITKVFSGNADLSGVTEEAPLKLKSAVHKAVLTIDEKGTAAAGAMFLERIPRSI 360
Db 301 SVLGQGITKVFSGNADLSGVTEEAPLKLKSAVHKAVLTIDEKGTAAAGAMFLERIPRSI 360

QY 361 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVNPQTOK 394
Db 361 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVNPQTOK 394
```

RESULT 3

```
US-11-050-926-286
; Sequence 286, Application US/11050926
; GENERAL INFORMATION:
; APPLICANT: Manjula GANNAVAPAPU
; APPLICANT: Sebastian HOERSCH
; APPLICANT: Shubhangi KAMAIKAR
; APPLICANT: Steve G. KOVATS
; APPLICANT: Rachel E. MEYERS
; APPLICANT: Michael MORRISSEY
; APPLICANT: Peter OLANDT
; APPLICANT: Ani SEN
; APPLICANT: Peter VEIBY
; APPLICANT: Gordon B. MILLS
; APPLICANT: Robert C. BAST, Jr.
; APPLICANT: Karen LU
; APPLICANT: Rosemarie SCHMANDT
; APPLICANT: Xumei ZHAO
; APPLICANT: Karen GLATT
; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
; FILE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
; FILE REFERENCE: MRI-030
; CURRENT APPLICATION NUMBER: US/11/050,926
; CURRENT FILING DATE: 2005-02-04
; PRIOR APPLICATION NUMBER: US/10/097,340
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 60/276,025
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/325,149
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/276,026
; PRIOR FILING DATE: 2001-03-14
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; PRIOR APPLICATION NUMBER: 60/324,967
; PRIOR FILING DATE: 2001/09/26
; PRIOR APPLICATION NUMBER: 60/311,732
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/325,102
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/323,580
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 286
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-050-926-286

Query Match      98.6%; Score 2003; DB 7; Length 418;
Best Local Similarity 98.5%; Pred. No. 1.4e-149;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDPOGDAQAOKTDTSHHQDHPFNKIPNLAEPFSLYRQLAHQSNSTNIFSPVSIATA 60
DB 25 EDPOGDAQAOKTDTSHHQDHPFNKIPNLAEPFSLYRQLAHQSNSTNIFSPVSIATA 84
QY 61 FAMLISLGTADTHDEILEGNFNLTOIPRAQIHGEGFQELLRTLNQDPSQLQTTGNGLFL 120
DB 85 FAMLISLGTADTHDEILEGNFNLTOIPRAQIHGEGFQELLRTLNQDPSQLQTTGNGLFL 144
QY 121 SOGLKLVDFLEDVKVLYHSEAFVNFQDTEQAQKQINDYVEKGTGQKIVDLVKELDRDT 180
DB 145 SEGKLVDFLEDVKVLYHSEAFVNFQDTEQAQKQINDYVEKGTGQKIVDLVKELDRDT 204
QY 181 VFALVNYIFFKGKWRPPEVKDTEBEDFHVQDVTTVKVPMMKRLGMFNIQHCKKLSWWL 240
DB 205 VFALVNYIFFKGKWRPPEVKDTEBEDFHVQDVTTVKVPMMKRLGMFNIQHCKKLSWWL 264
QY 241 LMKYLGNAITAIFFLPDEGKLOHLENELTHDIIITKFLNEDRRSASLHLPKLSITGTGYDLK 300
DB 265 LMKYLGNAITAIFFLPDEGKLOHLENELTHDIIITKFLNEDRRSASLHLPKLSITGTGYDLK 324
QY 301 SVLGQIGITKVFSGNADLSGVTEAPLKLKSAVHKAVLTIIDKGTGAAGAMFLERIPRSI 360
DB 325 SVLGQIGITKVFSGNADLSGVTEAPLKLKSAVHKAVLTIIDKGTGAAGAMFLERIPRSI 384
QY 361 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVNPQTK 394
DB 385 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVNPQTK 418

RESULT 5
US-60-685-372-1012
; Sequence 1012, Application US/60685372
; GENERAL INFORMATION:
; APPLICANT: Belouchi, Abdelmajid
; APPLICANT: Raelson, John V
; APPLICANT: Bradley, Walter E
; APPLICANT: Paquin, Bruno
; APPLICANT: Nguyen-Huu, Quynh
; APPLICANT: Croteau, Pascal
; APPLICANT: Allard, Rene
; APPLICANT: Little, Randall D
; APPLICANT: Cousineau, Johanne
; APPLICANT: Berdewegh, Paul V
; APPLICANT: Segal, Jonathan
; TITLE OF INVENTION: Genemap of the Human Genes Associated with Psoriasis
; FILE REFERENCE: 059908-5005-PR
; CURRENT APPLICATION NUMBER: US/60/685,372
; CURRENT FILING DATE: 2005-05-31
; NUMBER OF SEQ ID NOS: 2738
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1012
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-685-372-1012

Query Match      98.6%; Score 2003; DB 8; Length 418;
Best Local Similarity 98.5%; Pred. No. 1.4e-149;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDPOGDAQAOKTDTSHHQDHPFNKIPNLAEPFSLYRQLAHQSNSTNIFSPVSIATA 60
DB 25 EDPOGDAQAOKTDTSHHQDHPFNKIPNLAEPFSLYRQLAHQSNSTNIFSPVSIATA 84
QY 61 FAMLISLGTADTHDEILEGNFNLTOIPRAQIHGEGFQELLRTLNQDPSQLQTTGNGLFL 120
DB 85 FAMLISLGTADTHDEILEGNFNLTOIPRAQIHGEGFQELLRTLNQDPSQLQTTGNGLFL 144
QY 121 SOGLKLVDFLEDVKVLYHSEAFVNFQDTEQAQKQINDYVEKGTGQKIVDLVKELDRDT 180
DB 145 SEGKLVDFLEDVKVLYHSEAFVNFQDTEQAQKQINDYVEKGTGQKIVDLVKELDRDT 204
QY 181 VFALVNYIFFKGKWRPPEVKDTEBEDFHVQDVTTVKVPMMKRLGMFNIQHCKKLSWWL 240
DB 205 VFALVNYIFFKGKWRPPEVKDTEBEDFHVQDVTTVKVPMMKRLGMFNIQHCKKLSWWL 264

Query Match      98.6%; Score 2003; DB 8; Length 418;
Best Local Similarity 98.5%; Pred. No. 1.4e-149;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDPOGDAQAOKTDTSHHQDHPFNKIPNLAEPFSLYRQLAHQSNSTNIFSPVSIATA 60
DB 25 EDPOGDAQAOKTDTSHHQDHPFNKIPNLAEPFSLYRQLAHQSNSTNIFSPVSIATA 84
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QY 61 FAMLISLGTADTHDEILEGNFNLTOIPRAQIHGEGFQELLRTLNQDPSQLQTTGNGLFL 120
DB 85 FAMLISLGTADTHDEILEGNFNLTOIPRAQIHGEGFQELLRTLNQDPSQLQTTGNGLFL 144
QY 121 SOGLKLVDFLEDVKVLYHSEAFVNFQDTEQAQKQINDYVEKGTGQKIVDLVKELDRDT 180
DB 145 SEGKLVDFLEDVKVLYHSEAFVNFQDTEQAQKQINDYVEKGTGQKIVDLVKELDRDT 204
QY 181 VFALVNYIFFKGKWRPPEVKDTEBEDFHVQDVTTVKVPMMKRLGMFNIQHCKKLSWWL 240
DB 205 VFALVNYIFFKGKWRPPEVKDTEBEDFHVQDVTTVKVPMMKRLGMFNIQHCKKLSWWL 264
QY 241 LMKYLGNAITAIFFLPDEGKLOHLENELTHDIIITKFLNEDRRSASLHLPKLSITGTGYDLK 300
DB 265 LMKYLGNAITAIFFLPDEGKLOHLENELTHDIIITKFLNEDRRSASLHLPKLSITGTGYDLK 324
QY 301 SVLGQIGITKVFSGNADLSGVTEAPLKLKSAVHKAVLTIIDKGTGAAGAMFLERIPRSI 360
DB 325 SVLGQIGITKVFSGNADLSGVTEAPLKLKSAVHKAVLTIIDKGTGAAGAMFLERIPRSI 384
QY 361 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVNPQTK 394
DB 385 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVNPQTK 418

RESULT 5
US-60-685-372-1012
; Sequence 1012, Application US/60685372
; GENERAL INFORMATION:
; APPLICANT: Belouchi, Abdelmajid
; APPLICANT: Raelson, John V
; APPLICANT: Bradley, Walter E
; APPLICANT: Paquin, Bruno
; APPLICANT: Nguyen-Huu, Quynh
; APPLICANT: Croteau, Pascal
; APPLICANT: Allard, Rene
; APPLICANT: Little, Randall D
; APPLICANT: Cousineau, Johanne
; APPLICANT: Berdewegh, Paul V
; APPLICANT: Segal, Jonathan
; TITLE OF INVENTION: Genemap of the Human Genes Associated with Psoriasis
; FILE REFERENCE: 059908-5005-PR
; CURRENT APPLICATION NUMBER: US/60/685,372
; CURRENT FILING DATE: 2005-05-31
; NUMBER OF SEQ ID NOS: 2738
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1012
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-685-372-1012

Query Match      98.6%; Score 2003; DB 8; Length 418;
Best Local Similarity 98.5%; Pred. No. 1.4e-149;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDPOGDAQAOKTDTSHHQDHPFNKIPNLAEPFSLYRQLAHQSNSTNIFSPVSIATA 60
DB 25 EDPOGDAQAOKTDTSHHQDHPFNKIPNLAEPFSLYRQLAHQSNSTNIFSPVSIATA 84
QY 61 FAMLISLGTADTHDEILEGNFNLTOIPRAQIHGEGFQELLRTLNQDPSQLQTTGNGLFL 120
DB 85 FAMLISLGTADTHDEILEGNFNLTOIPRAQIHGEGFQELLRTLNQDPSQLQTTGNGLFL 144
QY 121 SOGLKLVDFLEDVKVLYHSEAFVNFQDTEQAQKQINDYVEKGTGQKIVDLVKELDRDT 180
DB 145 SEGKLVDFLEDVKVLYHSEAFVNFQDTEQAQKQINDYVEKGTGQKIVDLVKELDRDT 204
QY 181 VFALVNYIFFKGKWRPPEVKDTEBEDFHVQDVTTVKVPMMKRLGMFNIQHCKKLSWWL 240
DB 205 VFALVNYIFFKGKWRPPEVKDTEBEDFHVQDVTTVKVPMMKRLGMFNIQHCKKLSWWL 264
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QY 241 LMKYLGNATAIFPLPDEGKQLHLENLTHDIIITKFLNEDRRSASLHLPKLSITGTIDYDK 300
Db 265 LMKYLGNATAIFPLPDEGKQLHLENLTHDIIITKFLNEDRRSASLHLPKLSITGTIDYDK 324
QY 301 SVLGQIGITKVFSGNADLSGVTEAPLKLKSAVHKAVLIDKGTAAAGAMFLERIPRSI 360
Db 325 SVLGQIGITKVFSGNADLSGVTEAPLKLKSAVHKAVLIDKGTAAAGAMFLERIPMSI 384
QY 361 PPEVKENKPFVFLMIEQNTKSPFLFMGKVVNPTGK 394
Db 385 PPEVKENKPFVFLMIEQNTKSPFLFMGKVVNPTGK 418

RESULT 6
US-60-685-372-1014
; Sequence 1014, Application US/60685372
; GENERAL INFORMATION:
; APPLICANT: Belouchi, Abdelmajid
; APPLICANT: Raelson, John V
; APPLICANT: Bradley, Walter E
; APPLICANT: Paquin, Bruno
; APPLICANT: Nguyen-Huu, Quynh
; APPLICANT: Croteau, Pascal
; APPLICANT: Allard, Rene
; APPLICANT: Cousineau, Johanne
; APPLICANT: Berdewegh, Paul V
; APPLICANT: Segal, Jonathan
; TITLE OF INVENTION: Genemap of the Human Genes Associated with Psoriasis
; FILE REFERENCE: 059908-5005-PR
; CURRENT APPLICATION NUMBER: US/60/685,372
; CURRENT FILING DATE: 2005-05-31
; NUMBER OF SEQ ID NOS: 2738
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1014
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-685-372-1014

Query Match 98.6%; Score 2003; DB 8; Length 418;
Best Local Similarity 98.5%; Pred. No. 1.4e-149;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 EDPQGDAAQKTDTSHHDDQDHTFNKITPNLAEPFSLYRQLAHQSNSTNIFSPVSIATA 60
Db 25 EDPQGDAAQKTDTSHHDDQDHTFNKITPNLAEPFSLYRQLAHQSNSTNIFSPVSIATA 84
QY 61 FAMLISLGTAKDTHDEILEGLNFNLTQIPEAQIHEGFQELLRTLNQDPSQLQTTGNGLFL 120
Db 85 FAMLISLGTAKDTHDEILEGLNFNLTQIPEAQIHEGFQELLRTLNQDPSQLQTTGNGLFL 144
QY 121 SOGLKLVDKPLEVDKVLKLYHSEAPTVNFGDTEQAQKQINDYVEKGTQGKIVDLVKELDROT 180
Db 145 SEGKLVDKPLEVDKVLKLYHSEAPTVNFGDTEQAQKQINDYVEKGTQGKIVDLVKELDROT 204
QY 181 VFALVNYIFPKGWERPPEVKDTEEDFHVQDQVTVKVPMMKRLGMFNIQHCKKLSWWL 240
Db 205 VFALVNYIFPKGWERPPEVKDTEEDFHVQDQVTVKVPMMKRLGMFNIQHCKKLSWWL 264
QY 241 LMKYLGNATAIFPLPDEGKQLHLENLTHDIIITKFLNEDRRSASLHLPKLSITGTIDYDK 300
Db 265 LMKYLGNATAIFPLPDEGKQLHLENLTHDIIITKFLNEDRRSASLHLPKLSITGTIDYDK 324
QY 301 SVLGQIGITKVFSGNADLSGVTEAPLKLKSAVHKAVLIDKGTAAAGAMFLERIPRSI 360
Db 325 SVLGQIGITKVFSGNADLSGVTEAPLKLKSAVHKAVLIDKGTAAAGAMFLERIPMSI 384
QY 361 PPEVKENKPFVFLMIEQNTKSPFLFMGKVVNPTGK 394
Db 385 PPEVKENKPFVFLMIEQNTKSPFLFMGKVVNPTGK 418

RESULT 7
US-60-685-372-1016
; Sequence 1016, Application US/60685372
; GENERAL INFORMATION:
; APPLICANT: Belouchi, Abdelmajid
; APPLICANT: Raelson, John V
; APPLICANT: Bradley, Walter E
; APPLICANT: Paquin, Bruno
; APPLICANT: Nguyen-Huu, Quynh
; APPLICANT: Croteau, Pascal
; APPLICANT: Allard, Rene
; APPLICANT: Cousineau, Johanne
; APPLICANT: Berdewegh, Paul V
; APPLICANT: Segal, Jonathan
; TITLE OF INVENTION: Genemap of the Human Genes Associated with Psoriasis
; FILE REFERENCE: 059908-5005-PR
; CURRENT APPLICATION NUMBER: US/60/685,372
; CURRENT FILING DATE: 2005-05-31
; NUMBER OF SEQ ID NOS: 2738
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1016
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-685-372-1016

Query Match 98.6%; Score 2003; DB 8; Length 418;
Best Local Similarity 98.5%; Pred. No. 1.4e-149;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 EDPQGDAAQKTDTSHHDDQDHTFNKITPNLAEPFSLYRQLAHQSNSTNIFSPVSIATA 60
Db 25 EDPQGDAAQKTDTSHHDDQDHTFNKITPNLAEPFSLYRQLAHQSNSTNIFSPVSIATA 84
QY 61 FAMLISLGTAKDTHDEILEGLNFNLTQIPEAQIHEGFQELLRTLNQDPSQLQTTGNGLFL 120
Db 85 FAMLISLGTAKDTHDEILEGLNFNLTQIPEAQIHEGFQELLRTLNQDPSQLQTTGNGLFL 144
QY 121 SOGLKLVDKPLEVDKVLKLYHSEAPTVNFGDTEQAQKQINDYVEKGTQGKIVDLVKELDROT 180
Db 145 SEGKLVDKPLEVDKVLKLYHSEAPTVNFGDTEQAQKQINDYVEKGTQGKIVDLVKELDROT 204
QY 181 VFALVNYIFPKGWERPPEVKDTEEDFHVQDQVTVKVPMMKRLGMFNIQHCKKLSWWL 240
Db 205 VFALVNYIFPKGWERPPEVKDTEEDFHVQDQVTVKVPMMKRLGMFNIQHCKKLSWWL 264
QY 241 LMKYLGNATAIFPLPDEGKQLHLENLTHDIIITKFLNEDRRSASLHLPKLSITGTIDYDK 300
Db 265 LMKYLGNATAIFPLPDEGKQLHLENLTHDIIITKFLNEDRRSASLHLPKLSITGTIDYDK 324
QY 301 SVLGQIGITKVFSGNADLSGVTEAPLKLKSAVHKAVLIDKGTAAAGAMFLERIPRSI 360
Db 325 SVLGQIGITKVFSGNADLSGVTEAPLKLKSAVHKAVLIDKGTAAAGAMFLERIPMSI 384
QY 361 PPEVKENKPFVFLMIEQNTKSPFLFMGKVVNPTGK 394
Db 385 PPEVKENKPFVFLMIEQNTKSPFLFMGKVVNPTGK 418

RESULT 8
PCT-US05-07959-8
; Sequence 8, Application PC/TUS0507959
; GENERAL INFORMATION:
; APPLICANT: Arriva Pharmaceuticals, Inc.
; TITLE OF INVENTION: TREATMENT OF CHRONIC OBSTRUCTIVE PULMONARY DISEASE BY
; FILE REFERENCE: 39042-0020 PCT
; CURRENT APPLICATION NUMBER: PCT/US05/07959
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: U.S. 60/551,856
; PRIOR FILING DATE: 2004-03-09
; NUMBER OF SEQ ID NOS: 33


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; SEQ ID NO 8
; LENGTH: 503
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US05-07959-8

Query Match      98.6%; Score 2003; DB 1; Length 503;
Best Local Similarity 98.5%; Pred. No. 1.7e-149;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1  EDPOGDAQAQKTDTSHHDDQDHTFNKIPNLAEFAFSLYRQLAQHSNSTNIFSPVSIATA 60
Db 110 EDPOGDAQAQKTDTSHHDDQDHTFNKIPNLAEFAFSLYRQLAQHSNSTNIFSPVSIATA 169
QY 61  FAMLSTGKTADTHDEILEGLNFNLTOIPEAQIHEGFQELLRTLNQDPSQLQLTGNGLFL 120
Db 170 FAMLSTGKTADTHDEILEGLNFNLTOIPEAQIHEGFQELLRTLNQDPSQLQLTGNGLFL 229
QY 121 SOGLKLVDFLEVDVKKLYHSEAFVNFPGDTEAQAKQINDYVEKGTQCKIVDLVKELDRDT 180
Db 230 SEGKLVDFLEVDVKKLYHSEAFVNFPGDTEAQAKQINDYVEKGTQCKIVDLVKELDRDT 289
QY 181 VFALVNYIFFKGKWERPFVKDTEEDFHVQDQVTVTKVPMKRLGMFNIQHCCKLSSWVL 240
Db 290 VFALVNYIFFKGKWERPFVKDTEEDFHVQDQVTVTKVPMKRLGMFNIQHCCKLSSWVL 349
QY 241 LMKYLGNAITAIFFLPDEGKLOHLENELTHDIIITKFLNEDRRRSASLHLPKLSITGTGYDLK 300
Db 350 LMKYLGNAITAIFFLPDEGKLOHLENELTHDIIITKFLNEDRRRSASLHLPKLSITGTGYDLK 409
QY 301 SVLGQIGITKVFNSGADLSGVTTEAPLKLKSAVHKAVLTIDEKGTAAAGAMFLERIPRSI 360
Db 410 SVLGQIGITKVFNSGADLSGVTTEAPLKLKSAVHKAVLTIDEKGTAAAGAMFLERIPRSI 469
QY 361 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVNPQTOK 394
Db 470 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVNPQTOK 503

RESULT 9
PCT-US05-07959-16
; Sequence 16, Application PC/TUS0507959
; GENERAL INFORMATION:
; APPLICANT: Arriva Pharmaceuticals, Inc.
; TITLE OF INVENTION: TREATMENT OF CHRONIC OBSTRUCTIVE PULMONARY DISEASE BY
; FILE REFERENCE: 39042-0020 PCT
; CURRENT APPLICATION NUMBER: PCT/US05/07959
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: U.S. 60/551,856
; PRIOR FILING DATE: 2004-03-09
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 16
; LENGTH: 503
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US05-07959-16

Query Match      98.6%; Score 2003; DB 1; Length 503;
Best Local Similarity 98.5%; Pred. No. 1.7e-149;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1  EDPOGDAQAQKTDTSHHDDQDHTFNKIPNLAEFAFSLYRQLAQHSNSTNIFSPVSIATA 60
Db 2  EDPOGDAQAQKTDTSHHDDQDHTFNKIPNLAEFAFSLYRQLAQHSNSTNIFSPVSIATA 61
QY 61  FAMLSTGKTADTHDEILEGLNFNLTOIPEAQIHEGFQELLRTLNQDPSQLQLTGNGLFL 120
Db 62  FAMLSTGKTADTHDEILEGLNFNLTOIPEAQIHEGFQELLRTLNQDPSQLQLTGNGLFL 121
QY 121 SOGLKLVDFLEVDVKKLYHSEAFVNFPGDTEAQAKQINDYVEKGTQCKIVDLVKELDRDT 180
Db 122 SEGKLVDFLEVDVKKLYHSEAFVNFPGDTEAQAKQINDYVEKGTQCKIVDLVKELDRDT 181

; SEQ ID NO 8
; LENGTH: 503
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US05-07959-8

Query Match      98.6%; Score 2003; DB 1; Length 503;
Best Local Similarity 98.5%; Pred. No. 1.7e-149;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1  EDPOGDAQAQKTDTSHHDDQDHTFNKIPNLAEFAFSLYRQLAQHSNSTNIFSPVSIATA 60
Db 110 EDPOGDAQAQKTDTSHHDDQDHTFNKIPNLAEFAFSLYRQLAQHSNSTNIFSPVSIATA 169
QY 61  FAMLSTGKTADTHDEILEGLNFNLTOIPEAQIHEGFQELLRTLNQDPSQLQLTGNGLFL 120
Db 170 FAMLSTGKTADTHDEILEGLNFNLTOIPEAQIHEGFQELLRTLNQDPSQLQLTGNGLFL 229
QY 121 SOGLKLVDFLEVDVKKLYHSEAFVNFPGDTEAQAKQINDYVEKGTQCKIVDLVKELDRDT 180
Db 230 SEGKLVDFLEVDVKKLYHSEAFVNFPGDTEAQAKQINDYVEKGTQCKIVDLVKELDRDT 289
QY 181 VFALVNYIFFKGKWERPFVKDTEEDFHVQDQVTVTKVPMKRLGMFNIQHCCKLSSWVL 240
Db 290 VFALVNYIFFKGKWERPFVKDTEEDFHVQDQVTVTKVPMKRLGMFNIQHCCKLSSWVL 349
QY 241 LMKYLGNAITAIFFLPDEGKLOHLENELTHDIIITKFLNEDRRRSASLHLPKLSITGTGYDLK 300
Db 350 LMKYLGNAITAIFFLPDEGKLOHLENELTHDIIITKFLNEDRRRSASLHLPKLSITGTGYDLK 409
QY 301 SVLGQIGITKVFNSGADLSGVTTEAPLKLKSAVHKAVLTIDEKGTAAAGAMFLERIPRSI 360
Db 410 SVLGQIGITKVFNSGADLSGVTTEAPLKLKSAVHKAVLTIDEKGTAAAGAMFLERIPRSI 469
QY 361 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVNPQTOK 394
Db 470 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVNPQTOK 503

RESULT 10
US-11-077-276-8
; Sequence 8, Application US/11077276
; GENERAL INFORMATION:
; APPLICANT: Philip J. BARR
; APPLICANT: Philip PEMBERTON
; APPLICANT: Helen GIBSON
; TITLE OF INVENTION: TREATMENT OF CHRONIC OBSTRUCTIVE PULMONARY DISEASE BY
; FILE REFERENCE: 39042-0020
; CURRENT APPLICATION NUMBER: US/11/077,276
; CURRENT FILING DATE: 2005-03-09
; PRIOR APPLICATION NUMBER: U.S. 60/551,856
; PRIOR FILING DATE: 2004-03-09
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 8
; LENGTH: 503
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-077-276-8

Query Match      98.6%; Score 2003; DB 7; Length 503;
Best Local Similarity 98.5%; Pred. No. 1.7e-149;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1  EDPOGDAQAQKTDTSHHDDQDHTFNKIPNLAEFAFSLYRQLAQHSNSTNIFSPVSIATA 60
Db 110 EDPOGDAQAQKTDTSHHDDQDHTFNKIPNLAEFAFSLYRQLAQHSNSTNIFSPVSIATA 169
QY 61  FAMLSTGKTADTHDEILEGLNFNLTOIPEAQIHEGFQELLRTLNQDPSQLQLTGNGLFL 120
Db 170 FAMLSTGKTADTHDEILEGLNFNLTOIPEAQIHEGFQELLRTLNQDPSQLQLTGNGLFL 229
QY 121 SOGLKLVDFLEVDVKKLYHSEAFVNFPGDTEAQAKQINDYVEKGTQCKIVDLVKELDRDT 180
Db 230 SEGKLVDFLEVDVKKLYHSEAFVNFPGDTEAQAKQINDYVEKGTQCKIVDLVKELDRDT 289
QY 181 VFALVNYIFFKGKWERPFVKDTEEDFHVQDQVTVTKVPMKRLGMFNIQHCCKLSSWVL 240
Db 290 VFALVNYIFFKGKWERPFVKDTEEDFHVQDQVTVTKVPMKRLGMFNIQHCCKLSSWVL 349
QY 241 LMKYLGNAITAIFFLPDEGKLOHLENELTHDIIITKFLNEDRRRSASLHLPKLSITGTGYDLK 300
Db 350 LMKYLGNAITAIFFLPDEGKLOHLENELTHDIIITKFLNEDRRRSASLHLPKLSITGTGYDLK 409
QY 301 SVLGQIGITKVFNSGADLSGVTTEAPLKLKSAVHKAVLTIDEKGTAAAGAMFLERIPRSI 360
Db 410 SVLGQIGITKVFNSGADLSGVTTEAPLKLKSAVHKAVLTIDEKGTAAAGAMFLERIPRSI 469
QY 361 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVNPQTOK 394
Db 470 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVNPQTOK 503

RESULT 11
```

```
US-11-077-276-16
; Sequence 16, Application US/11077276
; GENERAL INFORMATION:
; APPLICANT: Philip J. BARR
; APPLICANT: Philip PEMBERTON
; APPLICANT: Helen GIBSON
; TITLE OF INVENTION: TREATMENT OF CHRONIC OBSTRUCTIVE PULMONARY DISEASE BY
; TITLE OF INVENTION: LOW DOSE INHALATION OF PROTEASE INHIBITOR
; FILE REFERENCE: 39042-0020
; CURRENT APPLICATION NUMBER: US/11/077,276
; CURRENT FILING DATE: 2005-03-09
; PRIOR APPLICATION NUMBER: U.S. 60/551,856
; PRIOR FILING DATE: 2004-03-09
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 16
; LENGTH: 503
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-077-276-16

Query Match
Best Local Similarity 98.6%; Score 2003; DB 7; Length 503;
Matches 388; Conservative 3; Mismatches 149; Indels 0; Gaps 0;

QY 1 EDPOGDAAKTDTSHHDQDHPFNKITPNLAFAFSLYRQLAHQSNSTNIFPSPVSIATA 60
DB 129 EDPOGDAAKTDTSHHDQDHPFNKITPNLAFAFSLYRQLAHQSNSTNIFPSPVSIATA 188
QY 61 FAMLSTGKTADTHDEILEGNFNLTOIPEAQIHEGFQELLRTLNQDPSQLQTTGNGLFL 120
DB 189 FAMLSTGKTADTHDEILEGNFNLTOIPEAQIHEGFQELLRTLNQDPSQLQTTGNGLFL 248
QY 121 SOGLKLVDFLEDKVLYHSEAFVNFVGTQEAQKQINDYVEKGTQGIKIVDLVKELDRDT 180
DB 249 SEGLKLVDFLEDKVLYHSEAFVNFVGTQEAQKQINDYVEKGTQGIKIVDLVKELDRDT 308
QY 181 VFALVNYIFFKGKWERPFVKDTEEDFHVDTQVTVKVPMMKRLGMFNIOHCKKLSWWL 240
DB 309 VFALVNYIFFKGKWERPFVKDTEEDFHVDTQVTVKVPMMKRLGMFNIOHCKKLSWWL 368
QY 241 LMKYLGNAITAIFFLPDEGKLOHLENLTHDIIITKFLNEDRRSASLHLPKLSITGTYDLK 300
DB 369 LMKYLGNAITAIFFLPDEGKLOHLENLTHDIIITKFLNEDRRSASLHLPKLSITGTYDLK 428
QY 301 SVLGQGITKTVFSNGADLSGVTEEAPLKLKSAVHKAVLTIDKGTAAAGAMFLERIPRSI 360
DB 429 SVLGQGITKTVFSNGADLSGVTEEAPLKLKSAVHKAVLTIDKGTAAAGAMFLERIPMSI 488
QY 361 PPEVKENKPFVFLMIEQNTKSPFLFMGKVVNPTOK 394
DB 489 PPEVKENKPFVFLMIEQNTKSPFLFMGKVVNPTOK 522

RESULT 13
PCT-US05-07959-20
; Sequence 20, Application PC/TUS0507959
; GENERAL INFORMATION:
; APPLICANT: Arriva Pharmaceuticals, Inc.
; TITLE OF INVENTION: TREATMENT OF CHRONIC OBSTRUCTIVE PULMONARY DISEASE BY
; TITLE OF INVENTION: LOW DOSE INHALATION OF PROTEASE INHIBITOR
; FILE REFERENCE: 39042-0020 PCT
; CURRENT APPLICATION NUMBER: PCT/US05/07959
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: U.S. 60/551,856
; PRIOR FILING DATE: 2004-03-09
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 20
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US05-07959-20

Query Match
Best Local Similarity 98.6%; Score 2003; DB 1; Length 522;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDPOGDAAKTDTSHHDQDHPFNKITPNLAFAFSLYRQLAHQSNSTNIFPSPVSIATA 60
DB 2 EDPOGDAAKTDTSHHDQDHPFNKITPNLAFAFSLYRQLAHQSNSTNIFPSPVSIATA 61
QY 61 FAMLSTGKTADTHDEILEGNFNLTOIPEAQIHEGFQELLRTLNQDPSQLQTTGNGLFL 120
DB 62 FAMLSTGKTADTHDEILEGNFNLTOIPEAQIHEGFQELLRTLNQDPSQLQTTGNGLFL 121
QY 121 SOGLKLVDFLEDKVLYHSEAFVNFVGTQEAQKQINDYVEKGTQGIKIVDLVKELDRDT 180
DB 122 SEGLKLVDFLEDKVLYHSEAFVNFVGTQEAQKQINDYVEKGTQGIKIVDLVKELDRDT 181
QY 181 VFALVNYIFFKGKWERPFVKDTEEDFHVDTQVTVKVPMMKRLGMFNIOHCKKLSWWL 240
DB 182 VFALVNYIFFKGKWERPFVKDTEEDFHVDTQVTVKVPMMKRLGMFNIOHCKKLSWWL 241
QY 241 LMKYLGNAITAIFFLPDEGKLOHLENLTHDIIITKFLNEDRRSASLHLPKLSITGTYDLK 300
DB 302 SVLGQGITKTVFSNGADLSGVTEEAPLKLKSAVHKAVLTIDKGTAAAGAMFLERIPMSI 361
QY 361 PPEVKENKPFVFLMIEQNTKSPFLFMGKVVNPTOK 394
DB 362 PPEVKENKPFVFLMIEQNTKSPFLFMGKVVNPTOK 395

RESULT 12
PCT-US05-07959-14
; Sequence 14, Application PC/TUS0507959
; GENERAL INFORMATION:
; APPLICANT: Arriva Pharmaceuticals, Inc.
; TITLE OF INVENTION: TREATMENT OF CHRONIC OBSTRUCTIVE PULMONARY DISEASE BY
; TITLE OF INVENTION: LOW DOSE INHALATION OF PROTEASE INHIBITOR
; FILE REFERENCE: 39042-0020 PCT
; CURRENT APPLICATION NUMBER: PCT/US05/07959
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: U.S. 60/551,856
; PRIOR FILING DATE: 2004-03-09
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 14
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US05-07959-14

Query Match
Best Local Similarity 98.6%; Score 2003; DB 1; Length 522;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDPOGDAAKTDTSHHDQDHPFNKITPNLAFAFSLYRQLAHQSNSTNIFPSPVSIATA 60
DB 129 EDPOGDAAKTDTSHHDQDHPFNKITPNLAFAFSLYRQLAHQSNSTNIFPSPVSIATA 188
QY 61 FAMLSTGKTADTHDEILEGNFNLTOIPEAQIHEGFQELLRTLNQDPSQLQTTGNGLFL 120
DB 189 FAMLSTGKTADTHDEILEGNFNLTOIPEAQIHEGFQELLRTLNQDPSQLQTTGNGLFL 248
QY 121 SOGLKLVDFLEDKVLYHSEAFVNFVGTQEAQKQINDYVEKGTQGIKIVDLVKELDRDT 180
DB 249 SEGLKLVDFLEDKVLYHSEAFVNFVGTQEAQKQINDYVEKGTQGIKIVDLVKELDRDT 308
QY 181 VFALVNYIFFKGKWERPFVKDTEEDFHVDTQVTVKVPMMKRLGMFNIOHCKKLSWWL 240
DB 309 VFALVNYIFFKGKWERPFVKDTEEDFHVDTQVTVKVPMMKRLGMFNIOHCKKLSWWL 368
QY 241 LMKYLGNAITAIFFLPDEGKLOHLENLTHDIIITKFLNEDRRSASLHLPKLSITGTYDLK 300
DB 369 LMKYLGNAITAIFFLPDEGKLOHLENLTHDIIITKFLNEDRRSASLHLPKLSITGTYDLK 428
QY 301 SVLGQGITKTVFSNGADLSGVTEEAPLKLKSAVHKAVLTIDKGTAAAGAMFLERIPRSI 360
DB 429 SVLGQGITKTVFSNGADLSGVTEEAPLKLKSAVHKAVLTIDKGTAAAGAMFLERIPMSI 488
QY 361 PPEVKENKPFVFLMIEQNTKSPFLFMGKVVNPTOK 394
DB 489 PPEVKENKPFVFLMIEQNTKSPFLFMGKVVNPTOK 522

RESULT 11
PCT-US05-07959-20
; Sequence 20, Application PC/TUS0507959
; GENERAL INFORMATION:
; APPLICANT: Arriva Pharmaceuticals, Inc.
; TITLE OF INVENTION: TREATMENT OF CHRONIC OBSTRUCTIVE PULMONARY DISEASE BY
; TITLE OF INVENTION: LOW DOSE INHALATION OF PROTEASE INHIBITOR
; FILE REFERENCE: 39042-0020 PCT
; CURRENT APPLICATION NUMBER: PCT/US05/07959
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: U.S. 60/551,856
; PRIOR FILING DATE: 2004-03-09
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 20
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US05-07959-20

Query Match
Best Local Similarity 98.5%; Score 2003; DB 1; Length 522;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDPOGDAAKTDTSHHDQDHPFNKITPNLAFAFSLYRQLAHQSNSTNIFPSPVSIATA 60
DB 129 EDPOGDAAKTDTSHHDQDHPFNKITPNLAFAFSLYRQLAHQSNSTNIFPSPVSIATA 188
QY 61 FAMLSTGKTADTHDEILEGNFNLTOIPEAQIHEGFQELLRTLNQDPSQLQTTGNGLFL 120
DB 189 FAMLSTGKTADTHDEILEGNFNLTOIPEAQIHEGFQELLRTLNQDPSQLQTTGNGLFL 248
QY 121 SOGLKLVDFLEDKVLYHSEAFVNFVGTQEAQKQINDYVEKGTQGIKIVDLVKELDRDT 180
DB 249 SEGLKLVDFLEDKVLYHSEAFVNFVGTQEAQKQINDYVEKGTQGIKIVDLVKELDRDT 308
QY 181 VFALVNYIFFKGKWERPFVKDTEEDFHVDTQVTVKVPMMKRLGMFNIOHCKKLSWWL 240
DB 309 VFALVNYIFFKGKWERPFVKDTEEDFHVDTQVTVKVPMMKRLGMFNIOHCKKLSWWL 368
QY 241 LMKYLGNAITAIFFLPDEGKLOHLENLTHDIIITKFLNEDRRSASLHLPKLSITGTYDLK 300
DB 369 LMKYLGNAITAIFFLPDEGKLOHLENLTHDIIITKFLNEDRRSASLHLPKLSITGTYDLK 428
QY 301 SVLGQGITKTVFSNGADLSGVTEEAPLKLKSAVHKAVLTIDKGTAAAGAMFLERIPRSI 360
DB 429 SVLGQGITKTVFSNGADLSGVTEEAPLKLKSAVHKAVLTIDKGTAAAGAMFLERIPMSI 488
QY 361 PPEVKENKPFVFLMIEQNTKSPFLFMGKVVNPTOK 394
DB 489 PPEVKENKPFVFLMIEQNTKSPFLFMGKVVNPTOK 522
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Db 242 LMKYLGNATAIFFLPDEGKLQHLLENELTHDIIITKFLNEDRRSASLHLPKLSITGYDLK 301
QY 301 SVLGQIGITKVFSGADLSGVTTEAPLKLKSAVHKAVLTIDKGTAAAGAMFLERIPRSI 360
Db 302 SVLGQIGITKVFSGADLSGVTTEAPLKLKSAVHKAVLTIDKGTAAAGAMFLERIPRSI 361
QY 361 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPTQK 394
Db 362 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPTQK 395

RESULT 14

US-11-077-276-14
; Sequence 14, Application US/11077276
; GENERAL INFORMATION:
; APPLICANT: Philip J. BARR
; APPLICANT: Philip PEMBERTON
; APPLICANT: Helen GIBSON
; TITLE OF INVENTION: TREATMENT OF CHRONIC OBSTRUCTIVE PULMONARY DISEASE BY
; TITLE OF INVENTION: LOW DOSE INHALATION OF PROTEASE INHIBITOR
; FILE REFERENCE: 39042-0020
; CURRENT APPLICATION NUMBER: US/11/077,276
; CURRENT FILING DATE: 2005-03-09
; PRIOR APPLICATION NUMBER: U.S. 60/551,856
; PRIOR FILING DATE: 2004-03-09
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 14
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-077-276-14

Query Match 98.6%; Score 2003; DB 7; Length 522;
Best Local Similarity 98.5%; Pred. No. 1.8e-149;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 EDPOGDAAKTDTSHHDQDHPFNKTPNLAEPFSLYRQLAHQSNSTNIFPSPVSIATA 60
Db 129 EDPOGDAAKTDTSHHDQDHPFNKTPNLAEPFSLYRQLAHQSNSTNIFPSPVSIATA 188
QY 61 FAMLISLGTAKADTHDEILEGLNFNLTOIPEAQIHEGFQELLRTLNQDPSQLQTTGNGLFL 120
Db 189 FAMLISLGTAKADTHDEILEGLNFNLTOIPEAQIHEGFQELLRTLNQDPSQLQTTGNGLFL 248
QY 121 SOGLKLVDFLEVDVKLYHSEAFVTNFGDTEQAQKQINDYVEKGTQGIKIVDLVKELDRDT 180
Db 249 SEGLKLVDFLEVDVKLYHSEAFVTNFGDTEQAQKQINDYVEKGTQGIKIVDLVKELDRDT 308
QY 181 VFALVNYIFPKGKWERPPEVKDTEBEDFHVDDVTVKVPMMKRLGMFNIOHCKKLSWVL 240
Db 309 VFALVNYIFPKGKWERPPEVKDTEBEDFHVDDVTVKVPMMKRLGMFNIOHCKKLSWVL 368
QY 241 LMKYLGNATAIFFLPDEGKLQHLLENELTHDIIITKFLNEDRRSASLHLPKLSITGYDLK 300
Db 369 LMKYLGNATAIFFLPDEGKLQHLLENELTHDIIITKFLNEDRRSASLHLPKLSITGYDLK 428
QY 301 SVLGQIGITKVFSGADLSGVTTEAPLKLKSAVHKAVLTIDKGTAAAGAMFLERIPRSI 360
Db 429 SVLGQIGITKVFSGADLSGVTTEAPLKLKSAVHKAVLTIDKGTAAAGAMFLERIPRSI 488
QY 361 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPTQK 394
Db 489 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPTQK 522

RESULT 15

US-11-077-276-20
; Sequence 20, Application US/11077276
; GENERAL INFORMATION:
; APPLICANT: Philip J. BARR
; APPLICANT: Philip PEMBERTON
; APPLICANT: Helen GIBSON
; TITLE OF INVENTION: TREATMENT OF CHRONIC OBSTRUCTIVE PULMONARY DISEASE BY

; TITLE OF INVENTION: LOW DOSE INHALATION OF PROTEASE INHIBITOR
; FILE REFERENCE: 39042-0020
; CURRENT APPLICATION NUMBER: US/11/077,276
; CURRENT FILING DATE: 2005-03-09
; PRIOR APPLICATION NUMBER: U.S. 60/551,856
; PRIOR FILING DATE: 2004-03-09
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 20
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-077-276-20

Query Match 98.6%; Score 2003; DB 7; Length 522;
Best Local Similarity 98.5%; Pred. No. 1.8e-149;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 EDPOGDAAKTDTSHHDQDHPFNKTPNLAEPFSLYRQLAHQSNSTNIFPSPVSIATA 60
Db 2 EDPOGDAAKTDTSHHDQDHPFNKTPNLAEPFSLYRQLAHQSNSTNIFPSPVSIATA 61
QY 61 FAMLISLGTAKADTHDEILEGLNFNLTOIPEAQIHEGFQELLRTLNQDPSQLQTTGNGLFL 120
Db 62 FAMLISLGTAKADTHDEILEGLNFNLTOIPEAQIHEGFQELLRTLNQDPSQLQTTGNGLFL 121
QY 121 SOGLKLVDFLEVDVKLYHSEAFVTNFGDTEQAQKQINDYVEKGTQGIKIVDLVKELDRDT 180
Db 122 SEGLKLVDFLEVDVKLYHSEAFVTNFGDTEQAQKQINDYVEKGTQGIKIVDLVKELDRDT 181
QY 181 VFALVNYIFPKGKWERPPEVKDTEBEDFHVDDVTVKVPMMKRLGMFNIOHCKKLSWVL 240
Db 182 VFALVNYIFPKGKWERPPEVKDTEBEDFHVDDVTVKVPMMKRLGMFNIOHCKKLSWVL 241
QY 241 LMKYLGNATAIFFLPDEGKLQHLLENELTHDIIITKFLNEDRRSASLHLPKLSITGYDLK 300
Db 242 LMKYLGNATAIFFLPDEGKLQHLLENELTHDIIITKFLNEDRRSASLHLPKLSITGYDLK 301
QY 301 SVLGQIGITKVFSGADLSGVTTEAPLKLKSAVHKAVLTIDKGTAAAGAMFLERIPRSI 360
Db 302 SVLGQIGITKVFSGADLSGVTTEAPLKLKSAVHKAVLTIDKGTAAAGAMFLERIPRSI 361
QY 361 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPTQK 394
Db 362 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPTQK 395

Search completed: June 20, 2005, 19:56:55

Job time : 67 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2005, 16:01:11 ; Search time 23 Seconds
(without alignments)
16.733 Million cell updates/sec

Title: US-09-885-914B-2

Perfect score: 21

Sequence: 1 RIPR 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 86

Minimum DB seq length: 0
Maximum DB seq length: 4

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : PIR 79:.*
1: PIR1:.*
2: PIR2:.*
3: PIR3:.*
4: PIR4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12	57.1	4	2 A02147	phagocytosis-stimu
2	10	47.6	4	2 I54357	schwannomin - mous
3	8	38.1	3	3 I78890	tyrosine protein k
4	7	33.3	3	3 RHSH	thyroliberin - she
5	7	33.3	3	3 A92571	thyroliberin - eas
6	7	33.3	3	3 RHTD	thyroliberin - Bom
7	7	33.3	3	3 A43391	TRH-like tripeptid
8	7	33.3	3	3 RHPGT	thyroliberin - pig
9	7	33.3	3	3 A33802	thyrotropin-releas
10	7	33.3	4	2 S53508	starvation-induced
11	7	33.3	4	2 A34626	RPCH-related neuro
12	7	33.3	4	2 I51049	metallothionein-A
13	7	33.3	4	2 PT0240	Ig heavy chain CRD
14	7	33.3	4	2 PL0140	carbon-monoxide de
15	7	33.3	4	2 S17255	ribosomal protein
16	7	33.3	4	2 PT0675	T-cell receptor be
17	7	33.3	4	2 PT0721	T-cell receptor be
18	7	33.3	4	2 A32039	tyrosine-melanocyt
19	6	28.6	4	2 I40804	endoglucanase F -
20	5	23.8	3	3 A22565	R-phycocerythrin al
21	5	23.8	3	3 PQ0010	angiotensin-conver
22	5	23.8	4	1 ECXAA	antho-RFamide neur
23	5	23.8	4	2 D41654	hypothetical prote
24	5	23.8	4	2 I40870	phospholipase C (S
25	5	23.8	4	2 A25844	antho-RF amide neu
26	5	23.8	4	2 I61883	protamine p1 - oxa
27	5	23.8	4	2 S47552	ubiquitin - rat
28	5	23.8	4	2 I37013	protamine p1 - Cer
29	5	23.8	4	2 I84439	protamine p1 - sav

30	5	23.8	4	2 A35779	neuropeptide Antho
31	5	23.8	4	2 A60418	FMRFamide - polych
32	5	23.8	4	2 ECNK	cardioexcitatory n
33	4	19.0	4	2 A61300	22K superhelical D
34	4	19.0	4	2 T46627	hypothetical prote
35	4	19.0	4	2 A27897	glucan 1,4-alpha-g
36	4	19.0	4	2 E44823	synptosomal-assoc
37	4	19.0	4	2 S09478	globulin IV alpha
38	4	19.0	4	2 PT0271	Ig heavy chain CRD
39	4	19.0	4	2 PT0633	T-cell receptor be
40	4	19.0	4	2 PT0551	T-cell receptor be
41	4	19.0	4	2 PT0697	phenol 2-monooxyge
42	3	14.3	4	2 A37832	cell surface adhes
43	3	14.3	4	2 B43848	hypothetical prote
44	3	14.3	4	2 I40505	hypothetical prote
45	3	14.3	4	2 T30569	COI intron 16 prot
46	3	14.3	4	2 I38888	hypothetical prote
47	3	14.3	4	2 A40135	branched-chain-ami
48	2	9.5	3	3 S13894	histidinol dehydro
49	2	9.5	3	3 E37196	bradykinin-potent
50	2	9.5	3	3 F37196	bradykinin-potent
51	2	9.5	3	3 T13892	cytochrome-c oxida
52	2	9.5	3	3 GKHU	growth-modulating
53	2	9.5	3	3 A60898	bursin - chicken
54	2	9.5	4	2 S18401	thyroglobulin - do
55	2	9.5	4	2 A48360	gamma subunit of P
56	2	9.5	4	2 S39390	myosin-light-chain
57	2	9.5	4	2 A53284	T-cell receptor be
58	2	9.5	4	2 A26209	protein-glutamine
59	2	9.5	4	2 PL0146	carbon-monoxide de
60	2	9.5	4	2 JQ1273	neuropeptide Antho
61	2	9.5	4	2 PT0645	T-cell receptor be
62	2	9.5	4	2 PT0534	T-cell receptor be
63	1	4.8	3	3 I50412	gene p20K protein
64	1	4.8	3	3 PT0578	T-cell receptor be
65	1	4.8	3	3 A23751	spinal cord peptid
66	1	4.8	3	3 B23751	spinal cord peptid
67	1	4.8	4	2 S43014	hypothetical prote
68	1	4.8	4	2 I57745	D-mannosate hydrol
69	0	0.0	3	3 PT0636	T-cell receptor be
70	0	0.0	3	3 PT0571	T-cell receptor be
71	0	0.0	3	3 PT0622	T-cell receptor be
72	0	0.0	3	3 S68328	blood cell protein
73	0	0.0	4	2 A41890	protein D - Escher
74	0	0.0	4	2 S43959	Ig mu chain V regi
75	0	0.0	4	2 B53284	T-cell receptor be
76	0	0.0	4	2 S55238	pallidipin - aasas
77	0	0.0	4	2 I40697	biotin A - Citroba
78	0	0.0	4	2 A32480	achatin-I - Giant
79	0	0.0	4	2 PT0696	T-cell receptor be
80	0	0.0	4	2 PT0711	T-cell receptor be
81	0	0.0	4	2 PT0661	T-cell receptor be
82	0	0.0	4	2 PT0712	T-cell receptor be
83	0	0.0	4	2 PT0698	T-cell receptor be
84	0	0.0	4	2 PT0677	T-cell receptor be
85	0	0.0	4	2 PT0706	T-cell receptor be
86	0	0.0	4	2 PT0566	T-cell receptor be

ALIGNMENTS

RESULT 1

A02147
phagocytosis-stimulating peptide (tuftsin) - human
C:Species: Homo sapiens (man)
C>Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C:Accession: A02147
R:Nishioaka, K.; Constantopoulos, A.; Satoh, P.S.; Najjar, V.A.
Biochem. Biophys. Res. Commun. 47, 172-179, 1972
A>Title: The characteristics, isolation and synthesis of the phagocytosis stimulating pei
A:Reference number: A02147; MUID:72187087; PMID:4112769
A:Accession: A02147

A:Molecule type: protein
A:Residues: 1-4 <NIS>
A:Cross-references: UNIPROT:P01858
A:Note: a peptide having the same structure, physical properties, and biological activities as thyroliberin - sheep
R:Fidalgo, B.V.; Najjar, V.A.
Biochemistry 6, 3386-3392, 1967
A:Residues: 1-4 <NIS>
A:Contents: annotation; immunoglobulin class
A:Comment: An IgG (called leukokinin) binds reversibly to the cell membrane of neutrophils. It is essential for maximum stimulation of the phagocytic activity of neutrophils.
C:Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 57.1%; Score 12; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PR 4
||
Db 3 PR 4

RESULT 2
I54357
Schwannomin - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C:Accession: I54357
R:Huyhn, D.P.; Nechiporuk, T.; Pulst, S.
Hum. Mol. Genet. 3, 1075-1079, 1994
A:Title: Alternative transcripts in the mouse neurofibromatosis type 2 (NF2) gene are controlled by a 5' upstream enhancer
A:Reference number: I54357; MUID:95072570; PMID:7981675
A:Accession: I54357
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-4 <RES>
A:Cross-references: GB:L28838; NID:G454836; PIDN:AAA57150.1; PID:G601923
C:Genetics:
A:Gene: NF2

Query Match 47.6%; Score 10; DB 2; Length 4;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 IP 3
:|
Db 1 VP 2

RESULT 3
I78890
tyrosine protein kinase - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C:Accession: I78890
R:Chow, L.M.; Davidson, D.; Fournel, M.; Gosselin, P.; Lemieux, S.; Lyu, M.S.; Kozak, C.
Oncogene 9, 3437-3448, 1994
A:Title: Two distinct protein isoforms are encoded by ntK, a csk-related tyrosine protein kinase
A:Reference number: I58407; MUID:95060800; PMID:7970703
A:Accession: I78890
A:Status: preliminary; translated from GB/EMBL/DDEJ
A:Molecule type: DNA
A:Residues: 1-3 <RES>
A:Cross-references: GB:L33339; NID:G609536; PIDN:AAA64432.1; PID:G609538
C:Genetics:
A:Gene: p52ntk

Query Match 38.1%; Score 8; DB 3; Length 3;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 IP 3
:|
Db 1 MP 2

RESULT 4

RHSHT

thyroliberin - sheep
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 09-Jul-2004
C:Accession: A93750; A01415
R:Desiderio Jr., D.M.; Burgus, R.; Dunn, T.F.; Vale, W.; Guillemin, R.; Ward, D.N.
Org. Mass Spectrom. 5, 221-228, 1971
A:Title: The elucidation of the primary structure of the hypothalamic thyroïd stimulating hormone

Query Match 33.3%; Score 7; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 P 3
|
Db 3 P 3

RESULT 5

A92971

thyroliberin - eastern newt (tentative sequence)
C:Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)
C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 09-Jul-2004
C:Accession: A92971; A01415
R:Grimm-Jorgensen, Y.; McKelvy, J.F.
J. Neurochem. 23, 471-478, 1974
A:Title: Biosynthesis of thyrotropin releasing factor by newt (Triturus viridescens) brain

Query Match 33.3%; Score 7; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 P 3
|
Db 3 P 3

Query Match 33.3%; Score 7; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 P 3
|
Db 3 P 3

RESULT 6

RHTDIO

thyroliberin - Bombina orientalis
C:Species: Bombina orientalis
C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 09-Jul-2004
C:Accession: A90919; A01415
R:Yasuhara, T.; Nakajima, T.

Query Match 33.3%; Score 7; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 P 3
|
Db 3 P 3

thyroliberin - Bombina orientalis
C:Species: Bombina orientalis
C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 09-Jul-2004
C:Accession: A90919; A01415
R:Yasuhara, T.; Nakajima, T.

Query Match 33.3%; Score 7; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 P 3
|
Db 3 P 3

RESULT 6

RHTDIO

thyroliberin - Bombina orientalis
C:Species: Bombina orientalis
C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 09-Jul-2004
C:Accession: A90919; A01415
R:Yasuhara, T.; Nakajima, T.

Query Match 33.3%; Score 7; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 P 3
|
Db 3 P 3

Chem. Pharm. Bull. 23, 3301-3303, 1975

A;Title: Occurrence of Pyr-His-Pro-NH-2 in the frog skin.

A;Reference number: A90919; MUID:76138399; PMID:815011

A;Accession: A90919

A;Molecule type: protein

A;Residues: 1-3 <VAS>

A;Cross-references: UNIPROT:P01151

C;Superfamily: thyroliberin

C;Keywords: amidated carboxyl end; cutaneous gland; hormone; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 33.3%; Score 7; DB 3; Length 3;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 P 3

DB 3 P 3

RESULT 7

A43391

TRH-like tripeptide - alfalfa

C;Species: Medicago sativa (alfalfa)

C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001

C;Accession: A43391

R;Lackey, D.B.

J. Biol. Chem. 267, 17508-17511, 1992

A;Title: Isolation and structural determination of a novel TRH-like tripeptide, pyroglu-

A;Reference number: A43391; MUID:92388092; PMID:1517203

A;Accession: A43391

A;Molecule type: protein

A;Residues: 1-3 <LAC>

C;Keywords: amidated carboxyl end; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 33.3%; Score 7; DB 3; Length 3;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 P 3

DB 3 P 3

RESULT 8

RHPGT

thyroliberin - pig

C;Species: Sus scrofa domestica (domestic pig)

C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Mar-2004

C;Accession: A01415

R;Nair, R.M.G.; Barrett, J.F.; Bowers, C.Y.; Schally, A.V.

Biochemistry 9, 1103-1106, 1970

A;Title: Structure of porcine thyrotropin releasing hormone.

A;Reference number: A90560; MUID:70136150; PMID:4984938

A;Accession: A01415

A;Molecule type: protein

A;Residues: 1-3 <NAI>

R;Boier, J.; Enzmann, F.; Folkers, K.; Bowers, C.Y.; Schally, A.V.

Biochem. Biophys. Res. Commun. 37, 705-710, 1969

A;Title: The identity of chemical and hormonal properties of the thyrotropin releasing h

A;Reference number: A90167; MUID:70039904; PMID:4982117

A;Contents: annotation

A;Note: biological activities and Rf values (in 17 chromatographic systems) of the synth

C;Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 33.3%; Score 7; DB 3; Length 3;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 P 3

DB 3 P 3

RESULT 9

A33802

thyrotropin-releasing hormone-like peptide - rabbit

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Mar-2004

C;Accession: A33802

R;Cockle, S.M.; Aitken, A.; Beg, F.; Smyth, D.G.

J. Biol. Chem. 264, 7788-7791, 1989

A;Title: A novel peptide, pyroglutamylglutamyproline amide, in the rabbit prostate comp

A;Reference number: A33802; MUID:89255196; PMID:2498305

A;Accession: A33802

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-3 <COC>

C;Keywords: amidated carboxyl end; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 33.3%; Score 7; DB 3; Length 3;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 P 3

DB 3 P 3

RESULT 10

S53508

starvation-induced ribonuclease - tomato

C;Species: Lycopersicon esculentum (tomato)

C;Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 07-May-1999

C;Accession: S53508

R;Koeck, M.; Loeffler, A.; Abel, S.; Glund, K.

Plant Mol. Biol. 27, 477-485, 1995

A;Title: cDNA structure and regulatory properties of a family of starvation-induced ribo

A;Reference number: S53506; MUID:95201242; PMID:7894013

A;Accession: S53508

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-4 <KOE>

Query Match 33.3%; Score 7; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 P 3

DB 2 P 2

RESULT 11

A34626

RPCH-related neuropeptide - ferruginous spindle

C;Species: Fusinus ferrugineus (ferruginous spindle)

C;Date: 06-Jul-1990 #sequence_revision 06-Jul-1990 #text_change 31-Dec-1993

C;Accession: A34626

R;Kuroki, Y.; Kanda, T.; Kubota, I.; Fujisawa, Y.; Ikeda, T.; Miura, A.; Minamitake, Y.;

Biochem. Biophys. Res. Commun. 167, 273-279, 1990

A;Title: A molluscan neuropeptide related to the crustacean hormone, RPCH.

A;Reference number: A34626; MUID:90179762; PMID:2310394

A;Accession: A34626

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-4 <KUR>

C;Keywords: neuropeptide

Query Match 33.3%; Score 7; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 P 3
|
Db 2 P 2

RESULT 12
I51049
metallothionein-A - rainbow trout (fragment)
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: I51049
R;Olsson, P.E.; Kling, P.; Erkel, L.J.; Kille, P.
Eur. J. Biochem. 230, 344-349, 1995
A;Title: Structural and functional analysis of the rainbow trout (Oncorhynchus mykiss) metallothionein-A
A;Reference number: I51049; MUID:95324545; PMID:7601121
A;Accession: I51049
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-4 <OLS>
A;Cross-references: EMBL:X80181; NID:g1019799; PIDN:CAA56466.1; PID:g4379328

Query Match 33.3%; Score 7; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 P 3
|
Db 3 P 3

RESULT 13
PT0240
IG heavy chain CRD3 region (clone 2-100B) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0240
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and joining in the human Ig heavy chain CRD3 region
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0240
A;Molecule type: DNA
A;Residues: 1-4 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match 33.3%; Score 7; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 P 3
|
Db 2 P 2

RESULT 14
PL0140
carbon-monoxide dehydrogenase (EC 1.2.99.2) large chain - Pseudomonas carboxydohydrogenans
C;Species: Pseudomonas carboxydohydrogenans
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: PL0140
R;Kraut, M.; Hugendieck, I.; Herwig, S.; Meyer, O.
Arch. Microbiol. 152, 335-341, 1989
A;Title: Homology and distribution of CO dehydrogenase structural genes in carboxydohydrogenans
A;Reference number: PL0138; MUID:90055678; PMID:2818128
A;Accession: PL0140
A;Molecule type: protein
A;Residues: 1-4 <KRA>
A;Cross-references: UNIPROT:P19916

C;Comment: Carbon-monoxide dehydrogenase consists of three polypeptide chains: large, medium, and small subunits.
C;Keywords: oxidoreductase

Query Match 33.3%; Score 7; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 P 3
|
Db 4 P 4

RESULT 15
S17255
ribosomal protein YmL1, mitochondrial, questionable - yeast (Saccharomyces cerevisiae) (f1)
C;Species: Saccharomyces cerevisiae
A;Variety: strain 07173
C;Date: 23-Apr-1993 #sequence_revision 14-Sep-1994 #text_change 09-Jul-2004
C;Accession: S17255
R;Grohmann, L.; Graack, H.R.; Kruff, V.; Choli, T.; Goldschmidt-Reisin, S.; Kitakawa, M.
FEBS Lett. 284, 51-56, 1991
A;Title: Extended N-terminal sequencing of proteins of the large ribosomal subunit from yeast
A;Reference number: S17255; MUID:91285106; PMID:2060626
A;Accession: S17255
A;Molecule type: protein
A;Residues: 1-4 <GRO>
A;Cross-references: UNIPROT:P36515
C;Comment: A coding region for this protein could not be identified in the genome of Saccharomyces cerevisiae
C;Genetics:
A;Genome: nuclear
C;Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 33.3%; Score 7; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 P 3
|
Db 4 P 4

Search completed: June 20, 2005, 16:34:35
Job time : 24 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2005, 15:59:16 ; Search time 109.5 Seconds
(without alignments)
18.706 Million cell updates/sec

Title: US-09-885-914B-2

Perfect score: 21

Sequence: 1 R1PR 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 26

Minimum DB seq length: 0

Maximum DB seq length: 4

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Uniprot 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	12	57.1	4	1 TUFT HUMAN	P01858 homo sapien
2	9	42.9	4	1 FYRI ANTEL	P58706 anthopleura
3	7	33.3	3	1 THYL BOMOR	P62970 bombina ori
4	7	33.3	3	1 THYL NOTVI	P62971 notophthalm
5	7	33.3	3	1 THYL_PIG	P62968 sus scrofa
6	7	33.3	3	1 THYL_SHEEP	P62969 ovis aries
7	7	33.3	4	1 DCML_PSECH	P19916 pseudomonas
8	7	33.3	4	1 YLMI YEAST	P36515 saccharomyc
9	7	33.3	4	2 Q16047	Q16047 homo sapien
10	5	23.8	4	1 FAR3 HIRME	P42562 hirudo medi
11	5	23.8	4	1 FLRF_HIRME	P42563 hirudo medi
12	5	23.8	4	1 FLRF_HIRME	P42561 hirudo medi
13	5	23.8	4	1 FLRF_HIRME	P42562 hirudo medi
14	5	23.8	4	1 FMRE MACNI	P01162 macrocallis
15	4	19.0	3	1 LUXE VIBFI	P24272 vibrio fisc
16	4	19.0	4	1 ILME SEPOF	P83568 sepiia offic
17	3	14.3	4	1 E0SI HUMAN	P02731 homo sapien
18	3	14.3	4	2 Q08433	Q08433 rattus sp.
19	2	9.5	3	1 GRWM HUMAN	P01157 homo sapien
20	2	9.5	4	1 DCMS_PSECH	P19918 pseudomonas
21	2	9.5	4	1 PFKA ANTEL	P58705 anthopleura
22	2	9.5	4	2 Q96A70	Q96A70 homo sapien
23	0	0.0	2	1 GWA SEPOF	P83570 sepiia offic
24	0	0.0	4	1 ACHI_ACHFU	P35904 achatina fu
25	0	0.0	4	1 OCP1_OCTMI	P58648 octopus min
26	0	0.0	4	1 OCP3_OCTMI	P58649 octopus min

ALIGNMENTS

```
RESULT 1
TUFT HUMAN STANDARD; PRT; 4 AA.
AC P01858;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Phagocytosis-stimulating peptide (tuftsin).
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72187087; PubMed=4112769;
RA Nishioka K., Constantopoulos A., Satoh P.S., Najjar V.A.;
RT "The characteristics, isolation and synthesis of the phagocytosis
stimulating peptide tuftsin.";
RL Biochem. Biophys. Res. Commun. 47:172-179(1972).
RN [2]
IMMUNOGLOBULIN CLASS.
RX MEDLINE=68091045; PubMed=4169272;
RA Fidalgo B.V., Najjar V.A.;
RT "The physiological role of the lymphoid system. VI. The stimulatory
effect of leucophilic gamma globulin (leucokinin) on the phagocytic
activity of human polymorphonuclear leucocyte.";
RL Biochemistry 6:3386-3392(1967).
CC -I- MISCELLANEOUS: An IGG (called leucokinin) binds reversibly to the
cell membrane of neutrophils in the blood. Leucokininase on the
membrane releases the active peptide tuftsin from the gamma chain.
CC Tuftsin is essential for maximum stimulation of the phagocytic
activity of neutrophils.
CC PIR; A02147; A02147.
DR MIM; 191150;
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006909; P:phagocytosis; NAS.
KW Direct protein sequencing.
SQ SEQUENCE 4 AA; 501 MW; 74176321C0000000 CRC64;

Query Match 57.1%; Score 12; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PR 4
Db 3 PR 4

RESULT 2
FYRI ANTEL STANDARD; PRT; 4 AA.
AC P58706;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Antho-Riamide I [Contains: Antho-Riamide II].
OS Anthopleura elegantissima (Sea Anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actinaria;
OC Nymphaeae; Actiniidae; Anthopleura.
OX NCBI_TaxID=6110;
RN [1]
RP SEQUENCE.
RX MEDLINE=92270459; PubMed=1821096; DOI=10.1016/0196-9781(91)90190-2;
RA Nothacker H.-P., Rinehart K.L. Jr., McFarlane I.D.;
RA Grimmelikhuijzen C.J.P.;
RT "Isolation of two novel neuropeptides from sea anemones: the unusual,
biologically active L-3-phenylalanyl-Tyr-Arg-Ile-NH2 and its des-
phenylalanyl fragment Tyr-Arg-Ile-NH2.";
RL Peptides 12:1165-1173(1991).
RN [2]
FUNCTION.
RP MEDLINE=93391436; PubMed=8397415;
RX McFarlane I.D., Hudman D., Nothacker H.-P., Grimmelikhuijzen C.J.P.;
```

RT "The expansion behaviour of sea anemones may be coordinated by two
 RL inhibitory neuropeptides, Antho-Kamide and Antho-Riamide.";
 RL Proc R. Soc. Lond. B, Biol. Sci. 253:183-188(1993).
 CC -1- FUNCTION: Inhibits spontaneous contractions in several muscle
 CC groups. May be involved in the expansion phase of feeding
 CC behaviour in sea anemones.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC TISSUE SPECIFICITY: Neuron specific.
 KW Amidation; Direct protein sequencing; Neuropeptide.
 FT CHAIN 1 4 Antho-Riamide I.
 FT CHAIN 2 4 Antho-Riamide II.
 FT MOD_RES 1 1 3-phenyllactic acid.
 FT MOD_RES 4 4 Isoleucine amide.
 SQ SEQUENCE 4 AA; 598 MW; 60441B59A0000000 CRC64;

Query Match 42.9%; Score 9; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RI 2
 ||
 3 RI 4

Db

RESULT 3

THYL_BOMOR STANDARD; PRT; 3 AA.

AC P62970; P01151;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Thyroliberin (Thyrotropin releasing hormone) (TRH) (Thyrotropin
 DE releasing factor) (TSH-releasing factor) (Protirelin).
 OS Bombina orientalis (Oriental fire-bellied toad).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
 OX NCBI_TaxID=8346;
 [1]
 RN TISSUE=Skin;
 RP SEQUENCE.
 RC MEDLINE=76138399; PubMed=815011;
 RA Yasuhara T., Nakajima T.;
 RT "Occurrence of Pyr-His-Pro-NH2 in the frog skin.";
 RL Chem. Pharm. Bull. 23:3301-3303(1975).
 CC -1- FUNCTION: TRH functions as a regulator of the biosynthesis of TSH
 CC in the anterior pituitary gland and as a neurotransmitter/
 CC neuromodulator in the central and peripheral nervous systems (By
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 DR PIR; A90919; RHTDTC.
 KW Amidation; Direct protein sequencing; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 Pyrrolidone carboxylic acid.
 FT MOD_RES 3 3 Proline amide.
 SQ SEQUENCE 3 AA; 380 MW; 7761F6B000000000 CRC64;

Query Match 33.3%; Score 7; DB 1; Length 3;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 P 3
 |
 3 P 3

Db

RESULT 4

THYL_NOTVI STANDARD; PRT; 3 AA.

AC P62971; P01151;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Thyroliberin (Thyrotropin releasing hormone) (TRH) (Thyrotropin
 DE releasing factor) (TSH-releasing factor) (Protirelin).

OS Notoptthalmus viridescens (Eastern newt) (Triturus viridescens).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Caudata; Salamandroidae; Salamandridae;
 OC Notoptthalmus.
 OX NCBI_TaxID=8316;
 [1]
 RN SEQUENCE.
 RP TISSUE=Brain;
 RC MEDLINE=75035605; PubMed=4214528;
 RA Grimm-Joergensen Y., McKelvy J.P.;
 RT "Biosynthesis of thyrotropin releasing factor by newt (Triturus
 RT viridescens) brain in vitro. Isolation and characterization of
 RT thyrotropin releasing factor.";
 RL J. Neurochem. 23:471-478(1974).
 CC -1- FUNCTION: TRH functions as a regulator of the biosynthesis of TSH
 CC in the anterior pituitary gland and as a neurotransmitter/
 CC neuromodulator in the central and peripheral nervous systems.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 DR PIR; A92971; A92971.
 KW Amidation; Direct protein sequencing; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 Pyrrolidone carboxylic acid.
 FT MOD_RES 3 3 Proline amide.
 SQ SEQUENCE 3 AA; 380 MW; 7761F6B000000000 CRC64;

Query Match 33.3%; Score 7; DB 1; Length 3;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 P 3
 |
 3 P 3

Db

RESULT 5

THYL_PIG STANDARD; PRT; 3 AA.

AC P62968; P01151;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Thyroliberin (Thyrotropin releasing hormone) (TRH) (Thyrotropin
 DE releasing factor) (TSH-releasing factor) (Protirelin).
 GN Name=TRH;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 [1]
 RN SEQUENCE.
 RP TISSUE=Hypothalamus;
 RC MEDLINE=70136150; PubMed=4984938;
 RA Nair R.M.G., Barrett J.F., Bowers C.Y., Schally A.V.;
 RT "Structure of porcine thyrotropin releasing hormone.";
 RL Biochemistry 9:1103-1106(1970).
 [2]
 RN SYNTHESIS.
 RP MEDLINE=70039904; PubMed=4982117;
 RC Boler J., Enzmann F., Folkers K., Bowers C.Y., Schally A.V.;
 RT "The identity of chemical and hormonal properties of the thyrotropin
 RT releasing hormone and pyroglutamyl-histidyl-proline amide.";
 RL Biochem. Biophys. Res. Commun. 37:705-710(1969).
 CC -1- FUNCTION: TRH functions as a regulator of the biosynthesis of TSH
 CC in the anterior pituitary gland and as a neurotransmitter/
 CC neuromodulator in the central and peripheral nervous systems.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 KW Amidation; Direct protein sequencing; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 Pyrrolidone carboxylic acid.
 FT MOD_RES 3 3 Proline amide.
 SQ SEQUENCE 3 AA; 380 MW; 7761F6B000000000 CRC64;

Query Match 33.3%; Score 7; DB 1; Length 3;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 P 3
|
Db 3 P 3

RESULT 6

THYL_SHEEP STANDARD; PRT; 3 AA.
AC P62969; P01151;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Thyroliberin (Thyrotropin releasing hormone) (TRH) (Thyrotropin releasing factor) (TSH-releasing factor) (Protirelin).
GN Names:TRH;
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE.
RC TISSUE=Hypothalamus;
RA Desiderio D.M. Jr., Burgess R., Dunn T.F., Vale W., Guillemin R., Ward D.N.;
RT "The elucidation of the primary structure of the hypothalamic thyroid stimulating hormone releasing factor of ovine origin by means of mass spectrometry.";
RL Org. Mass Spectrom. 5:221-228(1971).
RN [2]
RP SYNTHESIS.
RX MEDLINE=70163386; PubMed=4985794;
RA Burgess R., Dunn T.F., Desiderio D.M., Ward D.N., Vale W., Guillemin R.;
RT "Characterization of ovine hypothalamic hypophysiotropic TSH-releasing factor.";
RL Nature 226:321-325(1970).
CC -1- FUNCTION: TRH functions as a regulator of the biosynthesis of TSH in the anterior pituitary gland and as a neurotransmitter/neuromodulator in the central and peripheral nervous systems.
CC -1- SUBCELLULAR LOCATION: Secreted.
DR PIR; A93750; RSHST.
KW Amidation; Direct protein sequencing; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 Pyrrolidone carboxylic acid.
FT MOD_RES 3 3 Proline amide.
SQ SEQUENCE 3 AA; 380 MW; 7761F6B000000000 CRC64;

Query Match 33.3%; Score 7; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 P 3
|
Db 3 P 3

RESULT 7

DCML_PSECH STANDARD; PRT; 4 AA.
AC P19916;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Carbon monoxide dehydrogenase large chain (EC 1.2.99.2) (CO dehydrogenase subunit L) (CO-DH L) (Fragment).
GN Names:cutL;
OS Pseudomonas carboxydohydrogena.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Bradyrhizobiaceae.
OX NCBI_TaxID=290;
RN [1]
RP SEQUENCE.

RX MEDLINE=90055678; PubMed=2818128;
RA Kraut M., Hugendieck I., Herwig S., Meyer O.;
RT "Homology and distribution of CO dehydrogenase structural genes in carboxydotrophic bacteria.";
RL Arch. Microbiol. 152:335-341(1989).
CC -1- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon dioxide.
CC -1- CATALYTIC ACTIVITY: CO + H(2)O + A = CO(2) + AH(2).
CC -1- COFACTOR: Binds 1 copper(I) ion, 1 molybdenum(VI) ion and 1 molybdopterin cytosine dinucleotide (MCD) per subunit.
CC -1- SUBUNIT: Heterotrimer consisting of a large, a medium and a small subunit.
DR PIR; P01040; PLO140.
KW Direct protein sequencing; Molybdenum; Oxidoreductase.
FT NON_TER 4 4
SQ SEQUENCE 4 AA; 441 MW; 7761E876F0000000 CRC64;

Query Match 33.3%; Score 7; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 P 3
|
Db 4 P 4

RESULT 8

YLM1 YEAST STANDARD; PRT; 4 AA.
AC P365I5;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Mitochondrial 60S ribosomal protein L1 (YmL1) (Fragment).
GN Name=YmL1;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE.
RX MEDLINE=91285106; PubMed=2060626; DOI=10.1016/0014-5793(91)80759-V;
RA Grohmann L., Graack H.-R., Kruft V., Choli T., Goldschmidt-Reisin S., Kitakawa M.;
RT "Extended N-terminal sequencing of proteins of the large ribosomal subunit from yeast mitochondria.";
RL FEBS Lett. 284:51-56(1991).
CC -1- FUNCTION: Putative component of the large subunit of mitochondrial ribosome.
CC -1- SUBCELLULAR LOCATION: Mitochondrial.
DR PIR; S17255; S17255.
KW Direct protein sequencing; Mitochondrion; Ribosomal protein.
FT NON_TER 4 4
SQ SEQUENCE 4 AA; 402 MW; 7771B2D5D000000000 CRC64;

Query Match 33.3%; Score 7; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 P 3
|
Db 4 P 4

RESULT 9

Q16047 PRELIMINARY; PRT; 4 AA.
AC Q16047;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Interleukin 2 receptor alpha-subunit (fragment).
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92062171; PubMed=1840490;
 RA Marcken L., Moras V., Henon L., Lionne B., Bousseau A.,
 RA Daubry-Varsat A., Collins M., Mayaux J.F.;
 RT "An exon 5-deleted mRNA encodes a functional interleukin 2 receptor
 alpha-subunit.";
 RL Biochem. Biophys. Res. Commun. 180:1390-1395(1991).
 DR ENBL; S64248; AAB20279.1; -.
 DR HSSP; P01112; 1PLL.
 DR GO; GO:0005525; F:GTP binding; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0007264; P:small GTPase mediated signal transduction; IEA.
 DR InterPro; IPR001806; Ras_crisfmrng.
 DR PRINTS; PR00449; RASTRNSFRMNG.
 KW Receptor.
 FT NON TER.
 SQ SEQUENCE 4 AA; 525 MW; 69CAB769A0000000 CRC64;
 Query Match 33.3%; Score 7; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 P 3
 Db 2 P 2
 RESULT 10
 FAR3_HIRME STANDARD; PRT; 4 AA.
 AC P42562;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE FMRFamide-like neuropeptide YLRF-amide.
 OS Hirudo medicinalis (Medicinal leech)
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea;
 OC Arhynchobdellida; Hirudiniiformes; Hirudinidae; Hirudo.
 OX NCBI_TaxID=6421;
 RN [1]
 RP SEQUENCE
 RX MEDLINE=92195954; PubMed=1686933; DOI=10.1016/0196-9781(91)90035-N;
 RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
 RT "Identification of Rfamide neuropeptides in the medicinal leech.";
 RL Peptides 12:897-908(1991).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
 family.
 KW Amidation; Direct protein sequencing; Neuropeptide.
 FT MOD RES 4 4 Phenylalanine amide.
 SQ SEQUENCE 4 AA; 598 MW; 69D4073B30000000 CRC64;
 Query Match 23.8%; Score 5; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 R 1
 Db 3 R 3
 RESULT 11
 FAR4_HIRME STANDARD; PRT; 4 AA.
 AC P42563;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE FMRFamide-like neuropeptide YMRP-amide.

OS Hirudo medicinalis (Medicinal leech).
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea;
 OC Arhynchobdellida; Hirudiniiformes; Hirudinidae; Hirudo.
 OX NCBI_TaxID=6421;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92195954; PubMed=1686933; DOI=10.1016/0196-9781(91)90035-N;
 RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
 RT "Identification of Rfamide neuropeptides in the medicinal leech.";
 RL Peptides 12:897-908(1991).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
 family.
 KW Amidation; Direct protein sequencing; Neuropeptide.
 FT MOD RES 4 4 Phenylalanine amide.
 SQ SEQUENCE 4 AA; 616 MW; 69D4068B30000000 CRC64;
 Query Match 23.8%; Score 5; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 R 1
 Db 3 R 3
 RESULT 12
 FLRF_HIRME STANDARD; PRT; 4 AA.
 AC P42561;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE FLRFamide.
 OS Hirudo medicinalis (Medicinal leech), and
 OS Helisoma trivolvis (Snail).
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea;
 OC Arhynchobdellida; Hirudiniiformes; Hirudinidae; Hirudo.
 OX NCBI_TaxID=6421, 27815;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=H.medicalinalis;
 RX MEDLINE=92195954; PubMed=1686933; DOI=10.1016/0196-9781(91)90035-N;
 RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
 RT "Identification of Rfamide neuropeptides in the medicinal leech.";
 RL Peptides 12:897-908(1991).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=H.trivolvis; TISSUE=Kidney;
 RX MEDLINE=94286417; PubMed=7912428; DOI=10.1016/0196-9781(94)90166-X;
 RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
 RT "FMRFamide-related peptides from the kidney of the snail, Helisoma
 trivolvis.";
 RL Peptides 15:31-36(1994).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
 family.
 KW Amidation; Direct protein sequencing; Neuropeptide.
 FT MOD RES 4 4 Phenylalanine amide.
 SQ SEQUENCE 4 AA; 582 MW; 69D40729A0000000 CRC64;
 Query Match 23.8%; Score 5; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 R 1
 Db 3 R 3
 RESULT 13
 FLRN_ANTEL STANDARD; PRT; 4 AA.

AC P58707;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Antho-RNAmide.
 OS Anthopleura elegantissima (Sea anemone).
 OS Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
 OC Nynanthese; Actiniidae; Anthopleura.
 OX NCBI_TaxID=6110;
 RN
 RN SEQUENCE, AND MASS SPECTROMETRY.
 RX MEDLINE=90319122; PubMed=1973541;
 RA Grimmelikhuijzen C.J.P., Rinehart K.L. Jr., Jacob E., Graff D.,
 RA Reinscheid R.K., Nothacker H.-P., Staley A.L.;
 RT "Isolation of L-3-phenyllactyl-Leu-Arg-Asn-NH₂ (Antho-RNAmide), a sea
 RT anemone neuropeptide containing an unusual amino-terminal blocking
 RT group.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:5410-5414 (1990).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Neuron specific.
 CC -1- MASS SPECTROMETRY: MW=549.3; METHOD=FAB; RANGE=1-4; NOTE=Ref.1.
 DR PIR; A35779;
 KW Amidation; Direct protein sequencing; Neuropeptide.
 FT MOD_RES 1 1 3-phenyllactic acid.
 FT MOD_RES 4 4 Asparagine amide.
 SQ SEQUENCE 4 AA; 549 MW; 64540729A0000000 CRC64;
 Query Match 23.8%; Score 5; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 R 1
 DB 3 R 3
 RESULT 14
 FMRF_MACNI STANDARD; PRT; 4 AA.
 AC P01162;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE FMRFamide (Peak C) (Cardioexcitatory neuropeptide).
 OS Macrocallista nimbosa (Sun-ray clam),
 OS Nereis virens (Sandworm),
 OS Helisoma trivolvis (Medicinal leech), and
 OS Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroidea;
 OC Veneroidea; Veneridae; Macrocallista.
 OX NCBI_TaxID=6594, 6353, 6421, 27815;
 RN
 RN SEQUENCE, AND SYNTHESIS.
 RC SPECIES=M.nimbosa; TISSUE=Cerebral pedal, and Visceral ganglion;
 RX MEDLINE=77215956; PubMed=877582;
 RA Price D.A., Greenberg M.J.;
 RT "Structure of a molluscan cardioexcitatory neuropeptide.";
 RL Structure 197:670-671 (1977).
 RN
 RN SEQUENCE, AND CHARACTERIZATION.
 RC SPECIES=M.nimbosa; TISSUE=Ganglion;
 RX MEDLINE=78012038; PubMed=909875;
 RA Price D.A., Greenberg M.J.;
 RT "Purification and characterization of a cardioexcitatory neuropeptide
 RT from the central ganglia of a bivalve mollusc.";
 RL Prep. Biochem. 7:261-281 (1977).
 RN
 RN SEQUENCE.
 RC SPECIES=N.virens;
 RX MEDLINE=90259866; PubMed=2342992; DOI=10.1016/0196-9781(90)90113-J;
 RA Krajniak K.G., Price D.A.;
 RT "Authentic FMRFamide is present in the polychaete Nereis virens.";
 RL Peptides 11:75-77 (1990).

[4]
 RN SEQUENCE.
 RC SPECIES=H.medicalinalis;
 RX MEDLINE=92195954; PubMed=1686933; DOI=10.1016/0196-9781(91)90035-N;
 RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
 RT "Identification of RFamide neuropeptides in the medicinal leech.";
 RL Peptides 12:897-908 (1991).
 RN
 RN SEQUENCE.
 RC SPECIES=H.trivolvis; TISSUE=Kidney;
 RX MEDLINE=94286417; PubMed=7912428; DOI=10.1016/0196-9781(94)90166-X;
 RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
 RT "FMRFamide-related peptides from the kidney of the snail, Helisoma
 RT trivolvis.";
 RL Peptides 15:31-36 (1994).
 CC -1- FUNCTION: Myoactive; cardioexcitatory substance. Pharmacological
 CC activities include augmentation, induction, and regularization of
 CC cardiac contraction.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the FMRF (FMRFamide related peptide)
 CC family.
 DR PIR; A01426; ECKK.
 DR PIR; A60418; A60418.
 KW Amidation; Direct protein sequencing; Neuropeptide.
 FT MOD_RES 4 4 Phenylalanine amide.
 SQ SEQUENCE 4 AA; 600 MW; 69D40699A0000000 CRC64;
 Query Match 23.8%; Score 5; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 R 1
 DB 3 R 3
 RESULT 15
 LUXE_VIBFI STANDARD; PRT; 3 AA.
 AC P24272;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Long-chain-fatty-acid--luciferin-component ligase (EC 6.2.1.19) (Acyl-
 DE protein synthetase) (Fragment).
 GN Name=luxe;
 OS Vibrio fischeri.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrio.
 OX NCBI_TaxID=668;
 RN
 RN SEQUENCE FROM N.A.
 RP MEDLINE=91072226; PubMed=2254256;
 RA Swartzman E., Kapoor S., Graham A.F., Meighen E.A.;
 RT "A new Vibrio fischeri lux gene precedes a bidirectional termination
 RT site for the lux operon.";
 RL J. Bacteriol. 172:6797-6802 (1990).
 CC -1- FUNCTION: Acyl-protein synthetase activates tetradecanoic acid. It
 CC is a component of the fatty acid reductase complex responsible for
 CC converting tetradecanoic acid to the aldehyde which serves as
 CC substrate in the luciferase-catalyzed reaction.
 CC -1- CATALYTIC ACTIVITY: ATP + an acid + protein = AMP + diphosphate +
 CC an acyl-protein thioester.
 CC -1- PATHWAY: Bioluminescent fatty acid reduction system; second step.
 CC -1- SIMILARITY: Belongs to the luxe family.
 CC
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OM protein - protein search, using sw model

Run on: June 20, 2005, 14:16:51 ; Search time 113.5 Seconds
(without alignments)
13.630 Million cell updates/sec

Title: US-09-885-914B-2

Perfect score: 21

Sequence: 1 R1PR 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 19815

Minimum DB seq length: 0

Maximum DB seq length: 4

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp19808:*

2: Geneseqp19908:*

3: Geneseqp20008:*

4: Geneseqp20018:*

5: Geneseqp20028:*

6: Geneseqp20038:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	4	2	AAR59927
2	21	100.0	4	2	AAY44202
3	20	95.2	4	8	ADJ57388
4	19	90.5	4	5	AU78507
5	19	90.5	4	5	AU78526
6	17	81.0	4	8	ADK42152
7	16	76.2	4	2	AAR52385
8	16	76.2	4	2	AAR52384
9	16	76.2	4	2	AAR52383
10	16	76.2	4	2	AAY44204
11	16	76.2	4	2	AAY09581
12	16	76.2	4	2	AAY09582
13	16	76.2	4	2	AAY09580
14	16	76.2	4	7	ADC13966
15	16	76.2	4	8	ADG94025
16	16	76.2	4	8	ADI46295
17	16	76.2	4	8	ADP86600
18	16	76.2	4	8	ADSI14002
19	15	71.4	4	2	AAR65261
20	15	71.4	4	2	AAR86902
21	15	71.4	4	2	AAW21760
22	15	71.4	4	2	AAW75972
23	15	71.4	4	3	AAW94384
24	15	71.4	4	3	AB19559
25	15	71.4	4	3	AAI95742

26	15	71.4	4	4	AAE07853
27	15	71.4	4	4	AAE48691
28	15	71.4	4	5	AAW71247
29	15	71.4	4	5	AAU86935
30	15	71.4	4	5	AAU79240
31	15	71.4	4	6	ABG74124
32	15	71.4	4	6	ABP59998
33	15	71.4	4	6	ABG72040
34	15	71.4	4	6	AAE35823
35	15	71.4	4	6	ABR43318
36	15	71.4	4	6	AAE32090
37	15	71.4	4	6	ABG72334
38	15	71.4	4	6	ABR83547
39	15	71.4	4	7	ADC13980
40	15	71.4	4	8	ADG94151
41	15	71.4	4	8	ADJ46400
42	15	71.4	4	8	ADK71675
43	15	71.4	4	8	ADI46302
44	15	71.4	4	8	ADI46503
45	15	71.4	4	8	ADN48504
46	15	71.4	4	8	ADP86726
47	15	71.4	4	8	ADR38558
48	15	71.4	4	8	ADSI13999
49	15	71.4	4	8	ADSI13989
50	14	66.7	3	6	ABR43883
51	14	66.7	3	8	ADM01248
52	14	66.7	4	1	AAPI0134
53	14	66.7	4	2	AAR15327
54	14	66.7	4	2	AAR26423
55	14	66.7	4	2	AAR38137
56	14	66.7	4	2	AAW79354
57	14	66.7	4	2	AAW03144
58	14	66.7	4	2	AAW52360
59	14	66.7	4	2	AAW28140
60	14	66.7	4	2	AAW28143
61	14	66.7	4	2	AAW28142
62	14	66.7	4	2	AAW27998
63	14	66.7	4	2	AAW28141
64	14	66.7	4	2	AAW06088
65	14	66.7	4	2	AAW09557
66	14	66.7	4	3	AAW94546
67	14	66.7	4	5	AAU78864
68	14	66.7	4	5	AAE24415
69	14	66.7	4	5	AAE25916
70	14	66.7	4	5	ABG66063
71	14	66.7	4	5	ABG97617
72	14	66.7	4	5	AAO15382
73	14	66.7	4	7	ABR82527
74	14	66.7	4	7	ADC98013
75	14	66.7	4	7	ADL17647
76	14	66.7	4	8	ADG25097
77	14	66.7	4	8	ADG18987
78	14	66.7	4	8	ADK42346
79	14	66.7	4	8	ADK42347
80	14	66.7	4	8	ADQ33808
81	14	66.7	4	8	ADRO4663
82	14	66.7	4	8	ADRO4664
83	14	66.7	4	8	ADRO4507
84	14	66.7	4	8	ADRO4675
85	14	66.7	4	8	ADRO4662
86	14	66.7	4	8	ADRO4767
87	14	66.7	4	8	ADRO4687
88	14	66.7	4	8	ADRO4661
89	14	66.7	4	8	ADSI14001
90	13	61.9	4	2	AAW48072
91	13	61.9	4	2	AAE64131
92	13	61.9	4	2	AAW32851
93	13	61.9	4	2	AAW33405
94	13	61.9	4	3	AAW35836
95	13	61.9	4	4	AAU09059
96	13	61.9	4	5	ABG70627
97	13	61.9	4	6	ABP74896
98	13	61.9	4	6	AAE36043

Aae07853	Thrombin
Aab48691	Thrombin
Aab71247	Murine Ig
Aau86935	Immunoglob
Aau79240	Thrombin
Abg74124	Thrombin
Abp59998	Thrombin
Abg72040	Maltose b
Aae35823	Smac tetr
AbR43318	Thrombin
Aae32090	Expansin
Abg72334	Thrombin
AbR83547	Fusion pr
Adc13980	Rheumatol
Adg94151	Human JAM
Adj46400	Thrombin
Adk71675	Peptide c
Adi46302	Permeabil
Adi46503	Permeabil
Adn48504	M-Mulv re
Adp86726	Junctiona
Adr38558	Inhibitor
Adsi13999	Thrombin
Adsi13989	Thrombin
AbR43883	Synovial
Adm01248	Targeted
AAPI0134	Sequence
AAR15327	Tuftsia a
AAR26423	Immune en
AAR38137	Protease-
AAR79354	Human con
AAW03144	S. aureus
AAW52360	Beta-turn
AAW28140	Factor Xa
AAW28143	Factor Xa
AAW28142	Factor Xa
AAW27998	Factor Xa
AAW28141	Factor Xa
AAW06088	Archvilli
AAW94546	T. lanugin
AAU78864	Antimicro
AAE24415	Transport
AAE25916	Mouse and
ABG66063	Phage dip
ABG97617	Viral pep
AAO15382	Human Arf
ABR82527	Human apy
ADC98013	Signallin
ADL17647	MUPP PD27
ADG25097	Antimicro
ADG18987	Multimeri
ADK42346	Antibacte
ADK42347	Antibacte
ADQ33808	Tetrapept
ADRO4663	Factor XA
ADRO4664	Factor XA
ADRO4507	Factor XA
ADRO4675	Factor XA
ADRO4662	Factor XA
ADRO4767	Factor XA
ADRO4687	Factor XA
ADRO4661	Factor XA
ADSI14001	Thrombin
AAW48072	Biologica
AAE64131	Memory-ct
AAW32851	Protectin
AAW33405	Thrombin
AAW35836	T7 phage
AAU09059	Human thr
ABG70627	Human pro
ABP74896	Proteome
AAE36043	Cleavage

99 13 61.9 4 8 ADR49058 Caspase e
100 12 57.1 3 2 AAR30753 IGE-mast

ALIGNMENTS

RESULT 1
AAR5927
ID AAR5927 standard; peptide; 4 AA.

XX AAR5927;
AC
DT 25-MAR-2003 (revised)
DT 14-FEB-1995 (first entry)
XX
DE Alpha 1-antitrypsin Portland residues 355-358.

XX
KW Furin endopeptidase inhibitor; variant; bacterial infection;
KW AAT Portland.

XX Synthetic.

OS
PN WO9416073-A2.

XX
PD 21-JUL-1994.

XX
PF 07-JAN-1994; 94WO-US000247.

XX
PR 08-JAN-1993; 93US-00002202.

XX
PA (UYOR-) UNIV OREGON HEALTH SCI.

XX Thomas G, Anderson ED, Thomas L, Hayflick JS, Nelson J;
PI Stenglen SG;

XX WPI; 1994-249220/30.

XX
PT Furin endo;protease inhibitor to inhibit and treat bacterial and viral
PT infections - comprises an alpha-1 antitrypsin variant, pref. Portland.

XX Disclosure; Page 29; 42pp; English.

XX The sequence is that of alpha 1 antitrypsin Portland (AAT Portland)
CC residues 355-358 which is a furin endopeptidase inhibitor. The AAT
CC variant can be used to inhibit bacterial infections, esp. those caused by
CC Corynebacterium diphtheriae, Bacillus anthracis and Pseudomonas
CC aeruginosa, and to treat viral infections, esp. HIV and influenza.
CC (Updated on 25-MAR-2003 to correct PN field.)

XX
SQ Sequence 4 AA;

Query Match 100.0%; Score 21; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 R1PR 4
Db ||||
1 R1PR 4

RESULT 2
AAY44202
ID AAY44202 standard; protein; 4 AA.

XX AAY44202;

XX 25-JAN-2000 (first entry)

XX Reactive site loop of alphas-1-antitrypsin variant Portland.

XX Reactive site loop; RSL; alpha-1 antitrypsin variant Portland; PDX;
KW pharmacophore; guanidino residue; peptide mimetic; bacterial toxin;

KW furin recognition site; endoproteolytic activation;
KW endolytic maturation viral protein; bacterial infection; viral infection.
XX Synthetic.
OS Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 1 /note= "Wild type Ala substituted by Arg"

FT Misc-difference 4 /note= "Wild type Met substituted by Arg"

XX WO951624-A1.

XX 14-OCT-1999.

XX 08-APR-1999; 99WO-US007776.

XX 08-APR-1998; 98US-0081034P.

XX (UYOR-) UNIV OREGON HEALTH SCI.

XX Jean F, Thomas G;

XX WPI; 1999-620190/53.

XX New furin endoprotease inhibitor that mimics a specific region of alpha-1
PT antitrypsin Portland mutant, for treatment and prevention of bacterial
PT and viral infection.

XX Claim 1; Page 4; 108pp; English.

XX The present sequence is the reactive site loop of alpha-1 antitrypsin
CC mutated variant Portland (also termed PDX). This portion of the PDX
CC protein acts as the pharmacophore necessary for biological activity. The
CC RSL forms a rigid backbone having positively-charged guanidino residues
CC of each of the Arg residues extending in space away in the same direction
CC from the rest of the PDX protein. Peptides or peptide mimetics comprising
CC this sequence inhibit bacterial toxins that are processed at a consensus
CC furin recognition site, when administered in therapeutically effective
CC amounts. Endoproteolytic activation of bacterial toxins and endolytic
CC maturation of viral proteins is blocked by the peptide and peptide
CC mimetics. This is useful in treating infections of cells by bacteria and
CC viruses. It may also be used to inhibit processing of biologically active
CC proteins

XX Sequence 4 AA;

Query Match 100.0%; Score 21; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 R1PR 4
Db ||||
1 R1PR 4

RESULT 3
ADJ57388
ID ADJ57388 standard; peptide; 4 AA.

XX ADJ57388;

XX 06-MAY-2004 (first entry)

XX Peptide fragment of alpha-1-antitrypsin, use as convertase inhibitor.

XX Convertase; inhibitor; alpha-1-antitrypsin; antiinflammatory; vulnerary;
KW ophthalmological; dermatological; nephrotropic; hepatotropic;
KW vasotropic; antiinfertility; respiratory-gen.; cardiac; CNS-gen.;
KW cerebroprotective; neuroprotective; nootropic; cytostatic; antiarthritic;
KW antiarteriosclerotic.

OS Unidentified.
 PN WO2004009113-A1.
 XX
 PD 29-JAN-2004.
 XX
 PP 23-JUL-2003; 2003WO-GB003159.
 XX
 PR 24-JUL-2002; 2002GB-00017136.
 XX
 PA (RENO-) RENOVO LTD.
 XX
 PI Ferguson MWJ, Brunner G;
 XX
 DR WPI; 2004-180270/17.
 XX
 PT Use of a convertase inhibitor in the manufacture of a medicament for
 PT reducing scarring during the healing of wounds or reducing fibrosis in
 PT the treatment of fibrotic conditions.
 XX
 PS Disclosure; Page 10; 43pp; English.
 XX
 CC The present sequence is that of a peptide fragment of alpha-1-
 CC antitrypsin. Convertase inhibitors of the invention may be derivatives of
 CC alpha-1-antitrypsin comprising this sequence. The inventors have
 CC established that convertase enzymes act, both extracellularly and
 CC intracellularly, to cause the activation of latent transforming growth
 CC factor-beta (TGF-beta) in the extracellular space at the site of a wound
 CC of a fibrotic conditions. Thus, the present invention relates to use of
 CC convertase inhibitors for the reduction of scarring during the healing of
 CC wounds, for reducing fibrosis in the treatment of fibrotic conditions,
 CC for treating wounds to prevent scar formation, for preventing scarring of
 CC the eye, nervous tissue or intestines, dermal scarring and scarring
 CC following a burn. The fibrotic condition is a fibrotic disorder such as
 CC glomerulonephritis, cirrhosis of the liver, fibrocytic disease, adhesions
 CC and restenosis (all claimed). The convertase inhibitor can also be used
 CC for the treatment of hypertrophic and keloid scars, scarring in the heart,
 CC scarring of the gut, scarring in the pelvis in the region of the
 CC fallopian tubes leading to infertility, scarring following injury to the
 CC muscles, scarring or fibrosis following injury to tendons and ligaments,
 CC which can result in serious loss of function, liver fibrosis, pulmonary
 CC fibrosis, scleroderma, myocardial hibernation, fibrosis following a stroke
 CC myocardial infarction, central nervous system fibrosis following a stroke
 CC or neurodegenerative disorders (e.g. Alzheimer's disease), proliferative
 CC vitreoretinopathy, arthritis, arteriosclerosis and cancer.
 XX
 SQ Sequence 4 AA; .
 Query Match 95.2%; Score 20; DB 8; Length 4;
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 R1RP 4
 Db 1 RVP 4
 RESULT 4
 AAU78507
 ID AAU78507 standard; peptide; 4 AA.
 AC AAU78507;
 XX
 XX 18-JUN-2002 (first entry)
 DT
 XX BACE proprotein convertase cleavage site.
 DE
 XX Alzheimer's disease; beta amyloid precursor protein; BACE;
 KW beta-site APP cleaving enzyme; nontropic; neuroprotective;
 KW beta-site amyloid precursor protein (APP)-cleaving enzyme; APP;
 KW BACE secretase/sheddase; neurodegenerative disorder;
 KW proprotein convertase.
 XX

OS Unidentified.
 XX
 PN WO200210354-A2.
 XX
 PD 07-FEB-2002.
 XX
 PP 01-AUG-2001; 2001WO-CA001118.
 XX
 PR 01-AUG-2000; 2000CA-02313828.
 XX
 PA (RECL-) INST RECH CLINIQUES MONTREAL.
 XX
 PI Seidah NG, Chretien M, Cromlish JA;
 XX
 DR WPI; 2002-280632/32.
 XX
 PT Modulating activity of beta-site amyloid precursor protein-cleaving
 PT enzyme secretase/sheddase for treatment of neurodegenerative disorder
 PT characterized by generation of Abeta protein, by preventing cleavage of
 PT enzyme.
 XX
 PS Disclosure; Page 19; 64pp; English.
 XX
 CC This invention relates to a novel method for modulating activity of beta-
 CC site amyloid precursor protein (APP)-cleaving enzyme (BACE)
 CC secretase/sheddase. Cleavage of BACE by this enzyme results in the
 CC generation of a soluble BACE which enhances the production of the
 CC amyloidogenic peptide Abeta which has been shown to be involved in the
 CC aetiology of Alzheimer's disease. Inhibition of BACE secretase can be
 CC achieved by administration of an antisense nucleotide molecule capable of
 CC hybridising with BACE mRNA, by using a ribozyme that targets and degrades
 CC BACE secretase mRNA, with a peptide that can interfere with binding of
 CC the enzyme with BACE or using an antibody or antagonist that can function
 CC as an inhibitor of BACE secretase activation. The methods of the
 CC invention modulate the activity of BACE secretase/sheddase by preventing
 CC cleavage of BACE, which is useful for the treatment of a
 CC neurodegenerative disorder characterised by the generation of Abeta
 CC protein, especially Alzheimer's disease. The invention also comprises a
 CC method for identification of an agent that can alter the ability of BACE
 CC secretase to associate with and process a known substrate, this method
 CC can be used for high throughput screening of candidate molecules. The
 CC invention also comprises a method for determining whether an individual
 CC is at risk of developing a neurodegenerative disorder characterised by
 CC the generation of Abeta protein by measuring the levels of BACE C
 CC terminal cleavage products in a sample or tissue where an increase in
 CC cleavage products indicates a person at risk. The present sequence
 CC represents the BACE proprotein convertase cleavage site used to create
 CC the prosegment deletion mutants of the invention
 XX
 SQ Sequence 4 AA;
 Query Match 90.5%; Score 19; DB 5; Length 4;
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 R1RP 4
 Db 1 RLPR 4
 RESULT 5
 AAU78526
 ID AAU78526 standard; peptide; 4 AA.
 XX
 XX AAU78526;
 AC
 XX 18-JUN-2002 (first entry)
 DT
 XX RLPR proBACE cleavage site.
 DE
 XX Alzheimer's disease; beta amyloid precursor protein; BACE;
 KW beta-site APP cleaving enzyme; nontropic; neuroprotective;
 KW beta-site amyloid precursor protein (APP)-cleaving enzyme; APP;
 XX

KW BACE secretase/sheddase; neurodegenerative disorder.
 XX Unidentified.
 OS
 XX WO200210354-A2.
 FN
 XX 07-FEB-2002.
 PD
 XX 01-AUG-2001; 2001WO-CA001118.
 XX
 XX 01-AUG-2000; 2000CA-02313828.
 PF
 XX (RECL-) INST RECH CLINIQUES MONTREAL.
 PR
 XX Seidah NG, Chretien M, Cromlish JA;
 XX WPI; 2002-280632/32.
 DR
 XX
 XX Modulating activity of beta-site amyloid precursor protein-cleaving
 PT enzyme secretase/sheddase for treatment of neurodegenerative disorder
 PT characterized by generation of Abeta protein, by preventing cleavage of
 PT enzyme.
 PT
 XX Disclosure; Page 3; 64pp; English.
 PS
 XX This invention relates to a novel method for modulating activity of beta-
 CC site amyloid precursor protein (APP)-cleaving enzyme (BACE)
 CC secretase/sheddase. Cleavage of BACE by this enzyme results in the
 CC generation of a soluble BACE which enhances the production of the
 CC amyloidogenic peptide Abeta which has been shown to be involved in the
 CC aetiology of Alzheimer's disease. Inhibition of BACE secretase can be
 CC achieved by administration of an antisense nucleotide molecule capable of
 CC hybridising with BACE mRNA, by using a ribozyme that targets and degrades
 CC BACE secretase mRNA, with a peptide that can interfere with binding of
 CC the enzyme with BACE or using an antibody or antagonist that can function
 CC as an inhibitor of BACE secretase activation. The methods of the
 CC invention modulate the activity of BACE secretase/sheddase by preventing
 CC cleavage of BACE, which is useful for the treatment of a
 CC neurodegenerative disorder characterised by the generation of Abeta
 CC protein, especially Alzheimer's disease. The invention also comprises a
 CC method for identification of an agent that can alter the ability of BACE
 CC secretase to associate with and process a known substrate, this method
 CC can be used for high throughput screening of candidate molecules. The
 CC invention also comprises a method for determining whether an individual
 CC is at risk of developing a neurodegenerative disorder characterised by
 CC the generation of Abeta protein by measuring the levels of BACE C
 CC terminal cleavage products in a sample or tissue where an increase in
 CC cleavage products indicates a person at risk. The present sequence
 CC represents the RLPR cleavage site important for probACE processing
 XX
 SQ Sequence 4 AA;
 Query Match 90.5%; Score 19; DB 5; Length 4;
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 R1PR 4
 | : | |
 Db 1 RLPR 4
 RESULT 6
 ADK42152
 ID ADK42152 standard; peptide; 4 AA.
 XX
 AC ADK42152;
 XX
 XX 20-MAY-2004 (first entry)
 DT
 XX Antibacterial peptide from HBP #133.
 DE
 XX Human; heparin binding protein; HBP; neutrophil elastase; antibacterial;
 KW cytokine IL-6; monocyte; bacterial infection; sepsis; septic shock;
 KW

KW disseminated intravascular coagulation; meningococcal meningitis;
 KW pneumococcal pneumonia; inflammatory response; cell apoptosis;
 KW suppressed immune system; cancer; autoimmune diseases; trauma.
 XX
 OS Homo sapiens.
 XX
 XX WO2004016653-A2.
 PN
 XX 26-FEB-2004.
 PD
 XX 14-AUG-2003; 2003WO-DK000542.
 XX
 XX 15-AUG-2002; 2002DK-00001212.
 PR
 XX 19-AUG-2002; 2002US-0404155P.
 PR
 XX 27-JUN-2003; 2003DK-00000987.
 PR
 XX (LEUK-) LEUKOTOCH AS.
 PA
 XX Djurup R, Flodgaard HJ, Norris K;
 PI WPI; 2004-257185/24.
 XX
 XX New peptides of heparin-binding protein and/or human neutrophil elastase
 PT for manufacturing a medicament for the treatment of e.g. bacterial
 PT infections, disseminated intravascular coagulation, cancer or autoimmune
 PT diseases.
 PT
 XX Claim 52; SEQ ID NO 134; 211pp; English.
 PS
 XX The invention relates to an antibacterial peptide conforming to the
 CC generic peptide sequence appearing as ADK42632, the motif being derived
 CC from analysis of the protein sequences of human heparin binding protein,
 CC hHBP, pig pHBP and human neutrophil elastase (hNLE). Also included are a
 CC process for producing the new peptide (comprising providing an expression
 CC vector containing a DNA sequence encoding one or more of the above-
 CC mentioned amino acid sequences, transforming host cells with the vector,
 CC culturing the transformed host cells and purifying the expressed peptide),
 CC and a pharmaceutical composition comprising the new peptide. The peptide
 CC is capable of inhibiting or stimulating the secretion of cytokine IL-6
 CC from monocytes. The peptides are useful in manufacturing a medicament for
 CC the treatment of Gram-negative or Gram-positive bacterial infection, such
 CC as sepsis, severe sepsis, septic shock, disseminated intravascular
 CC coagulation, meningococcal meningitis or pneumococcal pneumonia. These
 CC may also be used in manufacturing a medicament for the stimulation or
 CC inhibition of inflammatory response, for the prevention of cell
 CC apoptosis, or for the treatment of individuals having suppressed immune
 CC system, cancer, autoimmune diseases and/or trauma. The present sequence
 CC represents an antibacterial peptide of the invention derived from human
 CC HBP.
 XX
 SQ Sequence 4 AA;
 Query Match 81.0%; Score 17; DB 8; Length 4;
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 R1PR 4
 | : | |
 Db 1 RPFR 4
 RESULT 7
 AAW52385
 ID AAW52385 standard; peptide; 4 AA.
 XX
 AC AAW52385;
 XX
 XX 01-JUL-1998 (first entry)
 DT
 XX Beta-turn region used in cyclic peptide of the invention.
 DE
 XX Beta-turn region; cyclic peptide; antimicrobial; disinfectant; therapy;
 KW preservative; amphipathic anti-parallel beta-sheet region; plant disease.
 KW

XX	Synthetic.
OS	WO9803192-A1.
XX	
PN	29-JAN-1998.
XX	
PD	
XX	
PF	23-JUL-1997; 97WO-US012974.
XX	
PR	24-JUL-1996; 96US-00685589.
XX	(INTR-) INTRABIOTICS PHARM INC.
PA	
XX	
PI	Chang C, Gu L, Chen J;
XX	
DR	WFI; 1998-120472/11.
XX	
PT	New cyclic peptide(s) with antimicrobial activity - contain amphipathic beta-sheet, loop and beta-turn regions, have better activity,
XX	bio:availability and protease resistance than linear analogues.
XX	
PS	Claim 3; Page 149; 160pp; English.
XX	
CC	This sequence represents a beta-turn region used in a peptide of the invention. The peptides are cyclic peptides (I), which have: (a) an amphipathic anti-parallel beta-sheet region (SR), a loop region (LR) and a beta-turn region (TR); (b) a net positive charge at physiological pH; and (c) at least one basic amino acid (aa) in LR or TR. (I) are broad spectrum antimicrobials, specifically for use against E. coli,
CC	Pseudomonas aeruginosa, methicillin-resistant Staphylococcus aureus (MRSA), vancomycin-resistant Enterococcus faecium and penicillin-resistant Streptococcus pneumoniae. More generally they are active against Gram-positive or -negative bacteria, fungi, yeast and protozoa.
CC	Apart from clinical uses, (I) are also used as disinfectants and preservatives for medical equipment, foods, cosmetics etc., also for treatment of plant diseases. Compared with non-cyclised analogues (i.e. tachyplesin and protergrin type peptides), (I) and are more effective, with better bioavailability and/or serum half-life (increased resistance to proteolysis). They are more suitable for oral administration, can be used at lower doses and are unlikely to induce development of resistant strains
XX	
SQ	Sequence 4 AA;
	Query Match 76.2%; Score 16; DB 2; Length 4;
	Best Local Similarity 100.0%; Pred. No. 1.8e+06;
	Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy	1 RIP 3
Db	
	1 RIP 3
RESULT 8	
ID	AAW52384
AC	AAW52384 standard; peptide; 4 AA.
XX	
XX	AAW52384;
DT	
XX	
DE	01-JUL-1998 (first entry)
XX	
KW	Beta-turn region used in cyclic peptide of the invention.
XX	
KW	Beta-turn region; cyclic peptide; antimicrobial; disinfectant; therapy;
XX	preservative; amphipathic anti-parallel beta-sheet region; plant disease.
OS	Synthetic.
XX	
PN	WO9803192-A1.
XX	
PD	
XX	
PF	29-JAN-1998.
XX	
PP	23-JUL-1997; 97WO-US012974.

XX New cyclic peptide(s) with antimicrobial activity - contain amphipathic
 PT beta-sheet, loop and beta-turn regions, have better activity,
 PT bio-availability and protease resistance than linear analogues.
 XX
 PS Claim 3; Page 148; 160pp; English.
 XX
 CC This sequence represents a beta-turn region used in a peptide of the
 CC invention. The peptides are cyclic peptides (I), which have: (a) an
 CC amphipathic anti-parallel beta-sheet region (SR), a loop region (LR) and
 CC a beta-turn region (TR); (b) a net positive charge at physiological pH;
 CC and (c) at least one basic amino acid (aa) in LR or TR. (I) are broad
 CC spectrum antimicrobials, specifically for use against *E. coli*,
 CC *Pseudomonas aeruginosa*, methicillin-resistant *Staphylococcus aureus*
 CC (MRSA), vancomycin-resistant *Enterococcus faecium* and penicillin-
 CC resistant *Streptococcus pneumoniae*. More generally they are active
 CC against Gram-positive or -negative bacteria, fungi, yeast and protozoa.
 CC Apart from clinical uses, (I) are also used as disinfectants and
 CC preservatives for medical equipment, foods, cosmetics etc., also for
 CC treatment of plant diseases. Compared with non-cyclised analogues (i.e.
 CC tachyplesin and protegrin type peptides), (I) and are more effective,
 CC with better bioavailability and/or serum half-life (increased resistance
 CC to proteolysis). They are more suitable for oral administration, can be
 CC used at lower doses and are unlikely to induce development of resistant
 CC strains
 XX
 SQ Sequence 4 AA;

Query Match 76.2%; Score 16; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RIP 3
 Db 1 RIP 3

RESULT 10
 AAY44204
 ID AAY44204 standard; protein; 4 AA.

XX AAY44204;
 AC
 XX 25-JAN-2000 (first entry)
 DT
 XX Generic sequence-2 of the reactive site loop of Portland protein.
 DE
 XX Reactive site loop; RSL; alpha-1 antitrypsin variant Portland; PDX;
 KW Portland protein; pharmacophore; guanidino residue; peptide mimetic;
 KW bacterial toxin; furin recognition site; endoproteolytic activation;
 KW endolytic maturation; viral protein; bacterial infection;
 KW viral infection.

XX Synthetic.
 OS
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT Misc-difference 2 /note= "Any amino acid residue"
 FT

PN WO9951624-A1.
 XX 14-OCT-1999.
 PD
 XX 08-APR-1999; 99WO-US007776.
 PF
 XX 08-APR-1998; 98US-0081034P.
 PR
 XX (UYOR-) UNIV OREGON HEALTH SCI.

XX Jean P, Thomas G;
 PI
 XX WPI; 1999-620190/53.
 DR

XX New furin endoprotease inhibitor that mimics a specific region of alpha-1
 PT antitrypsin Portland mutant, for treatment and prevention of bacterial
 PT and viral infection.
 XX
 PS Claim 1; Page 8; 108pp; English.
 XX
 CC The present sequence is the reactive site loop of alpha-1 antitrypsin
 CC mutated variant Portland (also termed PDX). This portion of the PDX
 CC protein acts as the pharmacophore necessary for biological activity. The
 CC RSL forms a rigid backbone having positively-charged guanidino residues
 CC from each of the Arg residues extending in space away in the same direction
 CC from the rest of the PDX protein. Peptides or peptide mimetics comprising
 CC this sequence inhibit bacterial toxins that are processed at a consensus
 CC furin recognition site, when administered in therapeutically effective
 CC amounts. Endoproteolytic activation of bacterial toxins and endolytic
 CC maturation of viral proteins is blocked by the peptide and peptide
 CC mimetics. This is useful in treating infections of cells by bacteria and
 CC viruses. It may also be used to inhibit processing of biologically active
 CC proteins
 XX
 SQ Sequence 4 AA;

Query Match 76.2%; Score 16; DB 2; Length 4;
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RIP 4
 Db 1 RXPR 4

RESULT 11
 AAY09581
 ID AAY09581 standard; peptide; 4 AA.

XX AAY09581;
 AC
 XX 21-JUL-1999 (first entry)
 DT
 XX Antimicrobial cyclic peptide beta-turn region SEQ ID NO:28.
 DE

XX Cyclic peptide; antimicrobial; amphiphilic beta-sheet; biostatic;
 KW biocidal; bacteria; yeast; *Candida* species; fungi; protozoa;
 KW *Escherichia coli*; *Pseudomonas aeruginosa*; infection; preservative;
 KW vancomycin-resistant *Enterococcus faecium*; disinfectant; food;
 KW methicillin-resistant *Staphylococcus aureus*; medical equipment;
 KW penicillin-resistant *Streptococcus pneumoniae*; cosmetic.

XX Synthetic.
 OS
 OS WO9921879-A1.

PN
 XX 06-MAY-1999.
 PD
 XX 27-OCT-1997; 97WO-US019557.
 PF
 XX 27-OCT-1997; 97WO-US019557.
 PR

PA (INTR-) INTRABIOTICS PHARM INC.
 XX
 XX Chang C, Gu L, Chen J;
 PI
 XX WPI; 1999-312941/26.
 DR

XX Antimicrobial cyclic peptides with amphiphilic beta-sheet region.
 XX
 PS Claim 3; Page 150; 167pp; English.

XX The present invention describes cyclic peptides (I): (i) comprising an
 CC amphiphilic anti-parallel beta-sheet region (A), a loop region (B) and a
 CC beta-turn (C); (ii) having net positive charge at physiological pH; and
 CC (iii) including at least one basic amino acid (aa) in (B) or (C).

CC AAY09554 to AAY09683 and AAY17301 to AAY17385 represent specifically
 CC claimed cyclic peptides and peptide segments. (I) are broad-spectrum
 CC antimicrobials (biostatic or biocidal), effective against bacteria, yeast
 CC (e.g. *Candida* species), fungi and protozoa. Particularly they are used to
 CC control *Escherichia coli*, *Pseudomonas aeruginosa*, vancomycin-resistant
 CC *Enterococcus faecium*, methicillin-resistant *Staphylococcus aureus* and
 CC penicillin-resistant *Streptococcus pneumoniae*. (A) are used to treat or
 CC prevent infections, in animals or plants, also as preservatives and
 CC disinfectants for medical equipment, foods, cosmetics, optionally as
 CC mixtures or in combination with other antimicrobials. Compared with
 CC linear analogues, (I) are more effective with better bioavailability
 CC and/or serum half-life (better resistance to proteolysis, allowing lower
 CC doses and making them more suitable for oral delivery). Since (I) are
 CC structurally related to naturally occurring antimicrobial peptides, they
 CC are less likely to induce development of resistant strains
 XX
 SQ Sequence 4 AA;

Query Match 76.2%; Score 16; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIP 3
 Db |||
 1 RIP 3

RESULT 12
 AAY09582
 ID AAY09582 standard; peptide; 4 AA.
 AC AAY09582;
 DT 21-JUL-1999 (first entry)
 DE Antimicrobial cyclic peptide beta-turn region SEQ ID NO:29.
 XX
 XX Cyclic peptide; antimicrobial; amphiphilic beta-sheet; biostatic;
 KW biocidal; bacteria; yeast; *Candida* species; fungi; protozoa;
 KW *Escherichia coli*; *Pseudomonas aeruginosa*; infection; preservative;
 KW vancomycin-resistant *Enterococcus faecium*; disinfectant; food;
 KW methicillin-resistant *Staphylococcus aureus*; medical equipment;
 KW penicillin-resistant *Streptococcus pneumoniae*; cosmetic.
 XX
 OS Synthetic.
 XX
 PN WO9921879-A1.
 XX
 PD 06-MAY-1999.
 XX
 PF 27-OCT-1997; 97WO-US019557.
 XX
 PR 27-OCT-1997; 97WO-US019557.
 XX
 XX (INTR-) INTRABIOTICS PHARM INC.
 PA
 PI Chang C, Gu L, Chen J;
 XX
 DR WPI; 1999-312941/26.
 XX
 PT Antimicrobial cyclic peptides with amphiphilic beta-sheet region.
 XX
 PS Claim 3; Page 150; 167pp; English.
 XX
 XX The present invention describes cyclic peptides (I): (i) comprising an
 CC amphiphilic anti-parallel beta-sheet region (A), a loop region (B) and a
 CC beta-turn (C); (ii) having net positive charge at physiological pH; and
 CC (iii) including at least one basic amino acid (aa) in (B) or (C).
 CC AAY09554 to AAY09683 and AAY17301 to AAY17385 represent specifically
 CC claimed cyclic peptides and peptide segments. (I) are broad-spectrum
 CC antimicrobials (biostatic or biocidal), effective against bacteria, yeast
 CC (e.g. *Candida* species), fungi and protozoa. Particularly they are used to
 CC control *Escherichia coli*, *Pseudomonas aeruginosa*, vancomycin-resistant

CC *Enterococcus faecium*, methicillin-resistant *Staphylococcus aureus* and
 CC penicillin-resistant *Streptococcus pneumoniae*. (A) are used to treat or
 CC prevent infections, in animals or plants, also as preservatives and
 CC disinfectants for medical equipment, foods, cosmetics, optionally as
 CC mixtures or in combination with other antimicrobials. Compared with
 CC linear analogues, (I) are more effective with better bioavailability
 CC and/or serum half-life (better resistance to proteolysis, allowing lower
 CC doses and making them more suitable for oral delivery). Since (I) are
 CC structurally related to naturally occurring antimicrobial peptides, they
 CC are less likely to induce development of resistant strains
 XX
 SQ Sequence 4 AA;

Query Match 76.2%; Score 16; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIP 3
 Db |||
 1 RIP 3

RESULT 13
 AAY09580
 ID AAY09580 standard; peptide; 4 AA.
 AC AAY09580;
 DT 21-JUL-1999 (first entry)
 DE Antimicrobial cyclic peptide beta-turn region SEQ ID NO:27.
 XX
 XX Cyclic peptide; antimicrobial; amphiphilic beta-sheet; biostatic;
 KW biocidal; bacteria; yeast; *Candida* species; fungi; protozoa;
 KW *Escherichia coli*; *Pseudomonas aeruginosa*; infection; preservative;
 KW vancomycin-resistant *Enterococcus faecium*; disinfectant; food;
 KW methicillin-resistant *Staphylococcus aureus*; medical equipment;
 KW penicillin-resistant *Streptococcus pneumoniae*; cosmetic.
 XX
 OS Synthetic.
 XX
 PN WO9921879-A1.
 XX
 PD 06-MAY-1999.
 XX
 PF 27-OCT-1997; 97WO-US019557.
 XX
 PR 27-OCT-1997; 97WO-US019557.
 XX
 XX (INTR-) INTRABIOTICS PHARM INC.
 PA
 PI Chang C, Gu L, Chen J;
 XX
 DR WPI; 1999-312941/26.
 XX
 PT Antimicrobial cyclic peptides with amphiphilic beta-sheet region.
 XX
 PS Claim 3; Page 150; 167pp; English.
 XX
 XX The present invention describes cyclic peptides (I): (i) comprising an
 CC amphiphilic anti-parallel beta-sheet region (A), a loop region (B) and a
 CC beta-turn (C); (ii) having net positive charge at physiological pH; and
 CC (iii) including at least one basic amino acid (aa) in (B) or (C).
 CC AAY09554 to AAY09683 and AAY17301 to AAY17385 represent specifically
 CC claimed cyclic peptides and peptide segments. (I) are broad-spectrum
 CC antimicrobials (biostatic or biocidal), effective against bacteria, yeast
 CC (e.g. *Candida* species), fungi and protozoa. Particularly they are used to
 CC control *Escherichia coli*, *Pseudomonas aeruginosa*, vancomycin-resistant
 CC *Enterococcus faecium*, methicillin-resistant *Staphylococcus aureus* and
 CC penicillin-resistant *Streptococcus pneumoniae*. (A) are used to treat or
 CC prevent infections, in animals or plants, also as preservatives and
 CC disinfectants for medical equipment, foods, cosmetics, optionally as
 CC mixtures or in combination with other antimicrobials. Compared with

CC linear analogues, (I) are more effective with better bioavailability
 CC and/or serum half-life (better resistance to proteolysis, allowing lower
 CC doses and making them more suitable for oral delivery). Since (I) are
 CC structurally related to naturally occurring antimicrobial peptides, they
 CC are less likely to induce development of resistant strains

XX
 SQ Sequence 4 AA;

Query Match 76.2%; Score 16; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIP 3
 |||
 Db 1 RIP 3

RESULT 14

ADG13966
 ID ADC13966 standard; peptide; 4 AA.

XX
 AC ADC13966;

XX
 DT 18-DEC-2003 (first entry)

XX Rheumatoid arthritis antibody detecting peptide SEQ ID NO:91.

XX autoantibody; rheumatoid arthritis; citrulline.

XX Synthetic.

XX WO2003050542-A2.

XX
 PD 19-JUN-2003.

XX
 PF 11-DEC-2002; 2002WO-NL000815.

XX
 PR 11-DEC-2001; 2001NL-01019540.

XX (TEWE-) STICHTING TECH WETENSCHAPPEN.

XX Van Ventrooij WJM, Drijfhout JW, Van Boekel MAM, Pruijn GJM;

XX WPI; 2003-663235/62.

XX Detecting autoantibodies from patients suffering from rheumatoid
 PT arthritis, by contacting a reactive peptide comprising citrulline residue
 PT or its analog with autoantibodies to form a complex, and detecting the
 PT complex.

XX Claim 8; SEQ ID NO 91; 110pp; English.

XX The invention relates to a novel method for detecting autoantibodies from
 CC patients suffering from rheumatoid arthritis. The method involves
 CC contacting autoantibodies with at least one reactive peptide comprising a
 CC citrulline residue or its analogue for a time sufficiently long to allow
 CC a complex to be formed between the autoantibody and peptide, and
 CC detecting the complex. The present sequence represents a peptide of the
 CC invention.

XX
 SQ Sequence 4 AA;

Query Match 76.2%; Score 16; DB 7; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IPR 4
 |||
 Db 2 IPR 4

RESULT 15

ADG94025

ID ADG94025 standard; peptide; 4 AA.

XX
 AC ADG94025;

XX
 DT 25-MAR-2004 (first entry)

XX Human JAM-1 permeabilising peptide SEQ ID NO:4.

XX human; permeabilising; interferon-beta; IFN-beta; mucosal delivery;

KW immunosuppressive; virucide; autoimmune disease; viral disease;

KW multiple sclerosis; chronic hepatitis B; condyloma acuminata;

KW papilloma virus; childhood viral encephalitis; wart.

XX Homo sapiens.

OS
 PN WO2004002404-A2.

XX
 PD 08-JAN-2004.

XX
 PF 18-JUN-2003; 2003WO-US019261.

XX
 PR 28-JUN-2002; 2002US-0393066P.

XX (NAST-) NASTECH PHARM CO INC.

XX Quay SC, Gupta M, De Meireles JC, Abd El- Shafy M;

XX WPI; 2004-122360/12.

XX Stable pharmaceutical composition comprising interferon compound(s)
 PT formulated for mucosal delivery to mammalian subjects in combination with
 PT mucosal delivery-enhancing agent(s).

XX Disclosure; SEQ ID NO 4; 353pp; English.

XX The invention relates to a novel stable pharmaceutical composition
 CC comprising one or more interferon (IFN)-beta compound(s) formulated for
 CC mucosal delivery to a mammalian subject in combination with one or more
 CC mucosal delivery-enhancing agent(s), where the composition following
 CC mucosal administration to the subject yields enhanced mucosal delivery of
 CC the one or more IFN-beta compound(s). A composition of the invention has
 CC immunosuppressive and virucide activity. The composition is useful for
 CC treating autoimmune diseases, viral disease, for alleviating one or more
 CC symptom(s) of multiple sclerosis (MS), chronic hepatitis B, condyloma
 CC acuminata, papilloma virus warts of the larynx or skin or childhood viral
 CC encephalitis in the subject without unacceptable adverse side effects.
 CC The composition can be delivered intranasally which reduces or eliminates
 CC compliance problems and side effects that attend delivery by injection.
 CC The sequences shown in ADG94022-ADG94810 represent permeabilising
 CC peptides used in a composition of the invention.

XX Sequence 4 AA;

Query Match 76.2%; Score 16; DB 8; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIP 3
 |||
 Db 2 RIP 4

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